

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 980

TO: Manjunath N Rao

Location: 1/10a11 & 10d01

Art Unit: 1652

Monday, July 07, 2003

Case Serial Number: 086082

From: Edward Hart

Location: Biotech-Chem Library

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Rao,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC-Biotech/ChemLib

1693

From:

Rao, Maniunath N.

Sent:

Wednesday, July 02, 2003 3:15 PM

To: Subject:

STIC-Biotech/ChemLib

Sequence search request for 10/086,082

From: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10D 01

Phone: 306-5681

Date: 7-2-03

Please search the following as soon as possible for application with serial number 10/086,082

- 1. SEQ ID NO:1, against all <u>commercial nucleic acid databases</u> including <u>issued patents database</u> and <u>pending application database</u> and provide a <u>print of all results</u>.
- 2. SEQ ID NO: 2 against all <u>commercial protein databases</u> including <u>issued patents database</u> and <u>pending</u> <u>application database</u> and provide a <u>print of all results</u>.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D. Biotechnology Patent Examiner Art Unit 1652, Room 10A11 Mail Box in 10D01 Crystal Mall 1, USPTO.

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Searcher:	
Phone:	
Location:	
Date Picked Up:	מכ
Searcher Prep/Review	2 5
Clerical:/_/	
Online time:	

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:______
DIALOG:____
Questel/Orbit:____
DRLink:____
Lexis/Nexis:_
Sequence Sys.:____
WWW/Internet:___
Other (specify):_____

STIC-Biotech/ChemLib

98001

ORFE

From:

Rao, Manjunath N.

Sent:

Wednesday, July 02, 2003 3:15 PM

To: Subject: STIC-Biotech/ChemLib Sequence search request for 10/086,082

From: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10D 01

Phone: 306-5681

Date: 7-2-03

Please search the following as soon as possible for application with serial number 10/086.082

1. SEQ ID NO:1, against all commercial nucleic acid databases including issued patents database and pending application database and provide a print of all results.

2. SEQ ID NO: 2 against all commercial protein databases including issued patents database and pending application database and provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D. Biotechnology Patent Examiner Art Unit 1652, Room 10A11 Mail Box in 10D01 Crystal Mall 1, USPTO.

> Point of Contact: Linda Basker

Library Technician CM1 1C19 Tel: 302-4500 1-1442 70-4500 2-328 aa

Phone:

Online time:

Edward Hair. Technical Into, Specialist STIC/Biotech

CMI 6802 Tel: 305-9205

Searcher: Location: Date Picked Up: Searcher Prep/Review Clerical:

TYPE OF SEARCH: NA Sequences: AA Sequences: Structures: Bibliographic: Litigation:_ Full text: Patent Family: Other:_

VENDOR/COST (where applic.) STN:

DIALOG:

Ouestel/Orbit:

DRLink: Lexis/Nexis:

Sequence Sys.: (7) WWW/Internet:_

Other (specify):



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Vol	untary Results Feedback Form
>	I am an examiner in Workgroup: Example: 1610
~	Relevant prior art found, search results used as follows:
	102 rejection
	103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Cor	nments:

Droportol/send completed forms to STIC/Blotech-Chem Library CM1 ∺ Girc⊁Desk :



Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

GenCore version 5.1.6 copyright (c) 1993 - 2003 Compuges Ltd.

OM protein - protein search, using sw model

July 3, 2003, 15:45:52; Search time 26 Seconds (Without alignments) 371.181 Million cell updates/sec Run on:

US-10-085-C82-2 1748 1 MKHI.EESIMAKRGVGAGRKP.........GNMVDPKYTVGAMINKNI.LV 328

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapex: 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

262574 seqs, 29422922 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

| /cgn2_6/ptodata1/iaa/5A_COMB.pep:*
| /cgn2_6/ptodata1/liaa/5B_COMB.pep:*
| /cgn2_6/ptodata1/liaa/6A_COMB.pep:*
| /cgn2_6/ptodata1/liaa/6B_COMB.pep:*
| /cgn2_6/ptodata1/liaa/pcTuts_COMB.pep:*
| /cgn2_6/ptodata1/liaa/pcTuts_COMB.pep:*
| /cgn2_6/ptodata1/liaa/pcTuts_COMB.pep:*
| /cgn2_6/ptodata1/liaa/pcackfiles1.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Describeron	Sequence 2, Appli	'n	ı,	Sequence 6. Appli	Š	:2	Sequence 2, Appl:	·	Sequence 198, App	۳.	7	-3	-:7	Sequence 4, Appli	77		Sequence 22, Appl	Sequence 22, Appl	Sequence 46. Appl	4	a)	Sequence 10, Appl	10,	7.0	A '.	Sequence 4, Appli	٠.
SOUTHINGS	ç		US-08-922-865-2	US-09-510-945-2	US-08-296-791-6	PCT-US95-10661A-6	US-08-926-8428-64	US-08-779-113-2	US-08-583-562B-2	35-09-556-877-180	US-09-620-412C-180	CS-09-177-165A-30	US-08-476-0628-42	PCT-US96-01314-42	US-07-978-895-4	US-08-473-119-4	115-08-475-352-4	5183884-4	853	US-08-914-848-22	US-09-413-814-46	CS-09-306-446C-2	US-08-484-438-9	US-08-369-822C-10	US-08-582-776C-10	-	US-09-171-337A-7	US-08-391-916A-4	5268290-2
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US-08-789-078-2	US-08-752-633-2	PCT-US95-04886-2	US-09-142-623-11	US-08-403-866-7	US-08-107-584B-10	US-08-107-684B-11	US-09-268-364-21	US-09-134-001C-4394	US-08-630-172-9	US-09-375-419-9	US-09-134-001C-5106	05-08-682-517-15	US-08-682-517-9	US-09-320-878-4	US-09-105-537-37	US-09-105-537-6	US-09-500-569-12
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AL IGNMENTS

RESULT 1 US-08-922-865-2 Sequence 2, Application US/08922865 Patent No. 60950616 GENERAL INFORMATION:	TITLE OF INVENTION: MICROGREANISM, LACTAMASE ENZYME OBTAINED TITLE OF INVENTION: THENEFROM, AND THEIR USE NUMBER OF SEQUENCES: 2 COMPOTER READABLE FORM: MEDIUM TYPE: FID OPPY GISH OFFICIAL OF THE OFFICE OFFICE OFFICE OFFI	COMPULES: 15M PC COMPULED COMPULES: 15M PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/922,865 FILING DATE:	INFORMATION FOR SECOND NO: 2: SEQUENCE CHARACIERISTICS: LENGTH: 575 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: Protein S-08-922-865-2	Owery Match Sest Local Similarity 24.0%; Pred. No. 3e-11: Matches 69; Conservative 33; Mismatches 85; Indels 101: Gaps 12:	39 PVSTPVLTIEPGDRIIVDTRDAEEGALNSDODIPS-CLIKMPFLN 82 1	83 PONGPIMVNSAEKGIVLAV	113 PYGICAMIPHFGGLIGTDLJAMLNDPLPEKVKMIKLDSEKVYWSKHITLFYKPHI 167 	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 177.5: DB 4: Length 575;
Pred. No. 3e-11;
3; Mismatches 85; Indexs 101
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Patent No. 624537

CENERAL INFORMATION:
APPLICANT: St. Geme III, Joseph W.
APPLICANT: Falkow, Stanley
TITLE OF INVENTION: Haemophilus Adherence and Penetration:
INUMBER OF ENUMENTION: Protein
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                             COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS COFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CUGRENT APPLICATION DATA: APPLICATION NUMBER: US/09/510,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred, No. 3e-1
33; Mismatches
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                    Sequence 2, Application US/09510949
Patent No. 6423522
GENERA, INPORMATION:
APPLICANT:
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MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
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Best Local Similarity 24.0%;
Matches 69; Conservative 33
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CITY: San Francisco
STATE: California
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GENERAL INFORMATION:
APPLICANT: Washington University, et al.
ITTLE OF INVENTION: Hoemophilus Adherence and Penetration Protein.
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                            Guery Match 5.2%, Score 91.5, DB 4: Length 1848; Best Local Similarity 19.1%, Pred. No. 1.4: Matches 73; Conservative 48: Mismatches 127; Indels 135;
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ADDRESSE: Flahr, Hobbach, Test, Albritton & Herbert STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STAIE: California
COUNTY: United States
2 TP: 94111-4187
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
303 CGKVRLGNMVDPKYTVGAMLNKN 325
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 KGTLSQDPLTNYAVLGDSGSPLFVYDREKGKWI,FLGSYDFWAGYNKKSWCEWNIY---- 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 LPNGIPMIDFSVVDVDKRIATLVNPQYVVGVKHVSNGVSEL--HFGNLNGN-----MNNS
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Patent No. 6030807
GENERAL INFORMATION:
APPLICANT: Sa-No. 6030807ueira, Isabel
APPLICANT: Generastre, Herminia
TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.2%; Score 91.5; DB 5; Length 1848;
19.1%; Pred. No. 1.4;
tive 48; Mismatches 127; Indels 135;
                                                            FILENO DATE: 10-700-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,791
FILING DATE: 25-80G-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
RECISTRATION NUMBER: 31.801
FECERENOCACKET NUMBER: FP-59941/RFT
TELECAMUNICATION INFORMATION:
TELECAMUNICATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10661A
FILING DATE: 16-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --KHEFAEKIYQQYSAGSLIGSN 356
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                                                                                                                                                                                                                                                                                                                                                                                                                   1848 amino acids
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Best Local Similarity 19.15
Best T3; Conservative
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SY: unknown
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US-08-926-842H-64
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193 VPDIGPGSITYPLVRAPGGRLFIGDAHACOGDGEICG--TAVEFASTTTIKVDLIKNWQL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 EKVRMIKLDSE-----KVYWSKRHTLPYKPHIGTLSVSPEIDSINSLTPONHGGNMD
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun,
STREET: 233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Staunton, Donald E. APPLICANT: Harris, Rdith S. ITILE OF INVENTION: Cytoplasmic Modulators of Integrin TITLE OF INVENTION: Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PARENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBIO
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vorsion #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                NAME: Jackson ESS., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/TOCKET NUMBER: 603-1-089 N
FELECHMUNICATION INFORMATION:
TELEPHOME: 201 487-5860
TELEFAX: 201 343-1584
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                                                                                                                                              APPLICATION NUMBER: US/08/926,842B
FILING DAIE: 10-SEP-1997
CLASSIFICATION: 435
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COUNTRY: United States of America
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US-08-779-113-2
Sequence 2, Application US/08779113
Patent No. 5948891
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.
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TELEX: 133521
INFORMATION FOR SEQ.
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acids
TOPE: Amino acids
TOPE: Amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
ORIGINAL SOURCE:
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US-09-556-877-180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 ----RVKESITRISRAPSVATVGSIC----DLNLKIPFINSSCMS-AHVISPSGRV 395
                                                                                                                                                                                                                                                                                                                                                                Match 4.7%, Score 82.5; DB 2; Length 857; Local Similarity 20.3%; Pred. No. 4.3; Local Similarity 21.3%; Pred. No. 4.3; Conservative 31; Mismatches 85; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Marray & Boran
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/06583562B
Patent, No. 5922570
GENERAL INFORMATION:
APPLICANT: Staunton, Donald
APPLICANT: Harris, Edith
ITILE OF INVENTION: Cytoplasmic Modulators of Integrin
ITILE OF INVENTION: Binding
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARCENTIN Release #1.6, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/583,5628
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                 FTLING DATE:
CLASSIPTCATION: 536
ATTCANEY/AGENT INDEMATION:
NAME: Greta E. No. 5948#91and
REGISTATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 278666/33773
TELECOMMUNICATION: INFORMATION:
APPLICATION NUMBER: US/08/779,113
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NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                              TELEFAX: 312.474-0448
IMPORMATION FOR SEQ ID NO: 2: SEQUENCE, CHARACTERISTICS: LENDIH: 857 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                         protein
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CLASSIFICATION: 536
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                                                                                                                                                                TELEPHONE:
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US-08-583-5628-2
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Matches
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271 YAKGELTIADSQEVLFSINKATKDGGAIFAEKDV-----SFENTTSLKVQTNGAEEKG 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 L...----EEIR-IKYNKAGTFETKKIT:.--PSLKAQASAGNADAWASSSPOSGSGA 413
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                                                                                                                                                                                                                                                                                                       5 EESIMAKR-----GVGAGRKPVTHHIJEEMOKEFHYTIGPYSTPVITIEPGUR- ---- 52
                                                                                                                                                                                                                                                                                                                                                              204 DEPCILKALPINHIGISFIPHEVGEHLVSIKKNGNHVANSPVSIMVVOSSIGGARRAKVY 26.3
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                                                                                                                                                                                                                                                                                                                                                                                                                    93 --------INVETRDAFEGAINSEQNIPSQLLKMPFLNPQNGFIMVNGAEKGNV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 KRHTLPYKPHIGTLSVSPEIDSINSLTPDNHGGNMDVPDIGPGSITYPLVRAFGGRU 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RVKES:TRTSRAPSVATVGSIC----DENLKIPEINSSDMS-AHVISPSGRV 395
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                              7.8.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEALECANT: Brobst. Peter
APPLICANT: Bhalia. A ay
APPLICANT: Skeiky, Vasir
APPLICANT: Skeiky, Steve
APPLICANT: Fing, Steve
APPLICANT: Fing, Steve
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 21012-44695
CURRENT APPLICATION NUMBER: US/09/556.877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.7%: Score 82.5; DB 4; Length 1752;
23.1%; Pred. No. 14:
Live 26: Mismatches 60; Indels 77.
                                                                                                                                                                                           Length 858,
                                                                                                                                                                                                                                                 85; Indels
                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                        4.7%; Score 82.5; DE
20.3%; Pred. No. 4.3;
Live 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 180, Application US/09556877
Patent No. 6432916
                           LENGIH: 858 amino acids TYPE: amino acid
                                                                                                                                                                         Guory Match
Best Local Similarity 20.3%
**** Age Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
SEQUENCE CHARACTERISTICS:
                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-583-5628-2
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Matches 49; Conserv
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; OKGANISM: C:lamydia
US-09-556-877-180
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73 SQLLKMPFLNPQNGP1MVNGAEKGDVLAVYIE·····SMLPRGVDPYGICAMIPHFGG 125
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                                                                                                                           578 DLQSGKCMHTF---NGRRLQRETQHTQTQSLGDKVAPIACVCIGDSE-CFSGDEFGCVKM 633
824 HLLSCGIDNT!KLWDVKTGKCIRTOFG-----BVEGVWDIAADNFR11SGSHDGSIKVW 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 VGAGRKPVTHHLTEEMQKEFH-YTIGPYSTPVETIEPGURIIVUTRDAFEGAINSEQDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; IGIGK----HFQTKESQETLHKFASKPASE------FVKILDTFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGENCE NO. 5877275
GENERAL INFORMATION:
APPLICANT: Arnaout. M. Amin
7.LTLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
1.TTLE OF INVENTION: SESPONSES WITH BETAZ INTEGRINS
1.TTLE OF CHOINNEES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUSA TITLE TO COMPATEL 18M COMPATER: ISM COMPATEL 6 OPERATING SYSTEM: Windows95 CSTATEM: Windows Version 2.0 CORENT APPLICATION DATA: APPLICATION NUMBER: 05/08/476,062A FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00786/066003
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                                                                                                                                                                                                                                                                                                                                                                                  US-08-476-062A-42; Sequence 42, Application US/U8476062A; Patent No. 5877275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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TELEX: 206154
INFORMATION FOR SEQ 1D NO.
SEQUENCE CEMERACTER: STICS:
LENGTH: 1170 amino acts
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FRAGMENT TYPE: internal
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 GAIYAKGDLSIQSSKOSLFNSNYSKQGGGALYVE----------GGINFOD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 LTAMENDPEPERVRMIKEDSEKVYWSKRHTEPYRPHIGTESVSPEIDSINSLIPENHGGN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 L------EEIR-IKYNKAGTFETKKITL---PSLKAQASAGNADAWASSSYQSGSA (11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 YSTPVLTTEPGDRIIVDTRDAFE--GAINSEODIPSOLLKMPFLNPQNGPIMVNGAE--- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tyers, Mike
APPLICANT: Fillems, Andrew
APPLICANT: Fillems, Andrew
APPLICANT: Fillems, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING USLIGHTING
TITLE OF INVENTION: DEPENDENT US/09/17/165A
CURRENT FILLNG DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 06/092,443
PRIOR APPLICATION NUMBER: 06/092,443
PRIOR FILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 30
                                                                                     GENERAL INFORMATION:

APPLICANT: SLEVEN P. Fling

APPLICANT: SLEVEN P. FLING

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IREAINENT AND

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121.46967

CURRENT APPLICATION NUMBER: 02009-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

ENGIH: 1752
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21.1%; Pred. No. 3;
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                        Sequence 180, Application US/09620412C
Patent No. 6448234
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ORGANISM: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.1
Matches 49; Conservative
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Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Chlamydia
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   US 09-620-412C-180
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Sequence 4, Application US/07978895
Patent No. 5480968
GENERAL INFORMATION:
APPLICANT: AATONSON, STRUCT A.
APPLICANT: AATONSON, STRUCT A.
TITLE OF INVENTION: AN ISCLATED POLYPEPTIDE RELATED TO THE
TITLE OF INVENTION: BLOASANS AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 12
COMMERS OF SEQUENCES: 12
COMMENS OF SEQUENCES: 12
ADDRESSEE: SAILE 400
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                                                                                        434 LLFQEPQGGGHWSQVQTIEGTQIGSYFGGELGGVDVDQDGETELLLIGAFLFYGEQRGGR 493
                                                                                                                                     213 JF1-----GDAHACQGD-GEICGTAVEFASITTIKVDLIKNWQLSWPRMENASNIMS 263
                                                                                                                                                                                 494 VFIYORRQLGFEEVSELQGDPGYFLG---RFGEAITALTDI--------NGFGLVD 538
377 F.-LDEKADLODDFFIGNEPLTPEVRAGYL-GYTVTWLPSROKTSLLASGAPRYOHMGKV 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 EQDIPSQLEKMP----PLNEQNGPIMVNGAEKGDVLAVYIESML-----PKGVS---
                                            171 SVSPE-----IDSINSLIPDNH-GGNMDVPDIG-PGSITYPLVRAP-----GGR
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SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/07/978,895
FILING DATE: 19921110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Rest Local Similarity 24.6%; Pred. No. 13:
Matches 52: Conservative 26: Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLING DALE ASSETS
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 37/444,406
FILING DATE: 01-DSC-1989
ATTORNEY/AGENT INFORMATION:
NAME: PEFFYMEN, DOX 33,435
KEGISTRATION NUMBER: 1414-028
TELEPHONE: (404) 688-9770
TELEPHONE: (404) 688-9860
INFORMATION FOR SECTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Suite 400
133 Carnegie Way, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) MOLECULE TYPE: protein
US-07-978-895-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                           IGSARPLED 272
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CPERATING SYSTEM:
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: U.S.A.
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SIATE: Georgia
COUNTRY: U.S.A.
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                             LFI------GDAHACOGD-GEICGTAVEFASTITIKVELIKNWQLSWPRMENAENIMS 263
  LIGIDLIAME------DPLPEKVRMIKLSSEKVYW--SKRRT------LPYKPH1GTE .70
                                                                                                                                       434 LLFQEPQGGGHWSQVQTIHGTQIGSYFGGELCGVDVDQFGETELLLIGAPLFYGHURGGR 493
                                                                                                                                                                                                                             494 VPIYORRQIGFEEVSELQGDPGYPLG ---REGHAITALTOI-------NGDGLVD 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 VCAGRKPVTHHLTEEMOKEEH-YTIGPYSTPVLIIEFGDRIIVDIRDAFEGAINSEQDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 IGIGK----HFQTKESQEJLHKFASKPASE------FVKILDTFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 SQLLKMPFLNPQNGPINVNGAEKGDVLAVYIE-----SMLPRGVDPYGICAMTEHFGG
                                                                                           171 SVSPE-----IDSINSLTPONH-GGNMEVPDIG-PGSITYPLVRAP- -----SGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: AFFHORS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFDIUM TYPE: 3.5" Diskette, 1.44 MD COMPUTER: IBM PS/Z Mcdel 502 or 555X OPPRATING SYSTEM: MS-DOS (Version 5.0) SCHWARE: MOTGPETECT (VERSION 5.1) CURRENT APPLICATION DATA: PCT/JS96/01314 FILLING DATE: 30-JAN-96 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 60786/267001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
AUDRESSEE: F'sh & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (617) 542-8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5" Dis
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Matches 70; Conser
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02113-2804
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kraus, Matthias H.
APPLICANT: Aaronson, Stuart A.
TITLE OF INVENTION: AN ISOLATED FOLYPEPTIDE RELATED TO THE
TITLE OF INVENTION: EPIDERMAL SKOWTH FACTOR RECEPTOR, ANIGEN THERETO, AND
TITLE OF INVENTION: BIOASSAYS AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 12
CORRESSIONIENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1036 ALSEPVGTLNRPRGSQSLLSPSSGYMPMNQGNLGESCQ---ESAVSGSSERCFRPVSLHP 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Feledse #1.0, Version #1.25
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/475,352
  1141 TPVTP-----LSPPGLSEEDVNGYVMPDTH 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 -PYKPHIGTLSVSP---EIDSINS-LIPDNH 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/444,406
FILING DATE: 01-DEC-1989
ATIORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE CPERATING SYSTEM: PC-DGS/MS-DGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/978,895
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Suite 400
STREET: 133 Carnegie Way, N.W.
                                                                                                           Sequence 4, Application US/08475352
Patent No. 5916755
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TELECCHMUNICATION INFORMATION:
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REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (404) 588-9880
INFORMATION FOR SEG ID NO: 4
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Best Local Similarity 24.6%
Matches 52; Conservative
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US-06-475-352-4
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                                                                                                                                                                                                     Sequence 4, Application US/08473119

Batent No. 5820859

GENERAL INFORMATION:
APPLICANT: Kraus, Matchias H.
APPLICANT: Aaronson, Stuart A.
TITLE OF INVENTION: EPIDERMAL GROWIH FACTOR RECEPTOR, ANTIGEN THERETO, AND TITLE OF INVENTION: BLASSAYS AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
APPLICANT OF NEW AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
1087 MPRGCLASESSEGEVIGSEA ---- FIQEKVSMCRSFSRSPRSPRGDSATHSORHSLL 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SCETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FLILIO DATE: US/C8/473,119
FLILIO DATE: US/UN-1995
CLASSIFICATION: 424
                                                                                               1141 TPVTP-----LSPPGLEERDVNGYVM9UTH 1165
                                                                  162 -PYKPHIGTLSVSP---EIDSINS-LIPDNH 187
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APPLICATION NUMBER: 07/976,895
FILING DATE: 10.NOV-1992
FILING DATE: 01.ORD 07/444,406
FILING DATE: 01.ORD 1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ferryman, David 3.
REGISTRATION NUMBER: 33.438
REFERENCE/DOCKET NUMBER: 1414-028
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 Carnegie Way, N.W.
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(404) 688-9880
R SEQ ID NO: 4:
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Query Match
Best Local Similarity 24.69
Matches 52: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite 400
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MEDIUM TYPE: Floppy
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                                                                                                                                                                             RESULT 14
US-08-473-119-4
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Tel: +55-11-2704922
Fax: +55-11-270700.
Fax: +55-11-270700.
Fax: by the sequence of the sequence was derived from the FAPESP/LICR Human Cancer Geneme Project. This sequence was derived from the following URL (http://www.ludwiq.org.br/scripts/gethtml2.pl?ti=RC2&t2-RC2-HT0275-01199-011-f11&t3=1999-11-01&t4*1)
Seq primer: puc 18 forward
High quality sequence start: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Lidvig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP.
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TITLE
JOURNAL
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AWAROERH
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KEYWORDS
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compuged Ltd.
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AW380638 RC2-HT027 BM615374 17000687; AV551507 AV551567 BM582997 170006872 AL064465 Drosophil AV629284 AV629284

BM615374 AV551507 BM582997 CNS0037Q AV629284

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AGE 1012 HS 1010 AGE 1013 AGE 1013
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BHY09682 WOMELCTF
AA026735 Ze65810.S
H76593 Yu65104.1:
AA019639 Ze6261.S
AA01557 Ze646406.S
R6854211 35249 WA
B57961 CLT.HSP-201
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BJ246954 BJ246954
BJ234037 BJ234037
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MRNA sequence.
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HS_5103_A
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases : to 280)
HGGP http://www.ludwig.org.br/ORESTES.
The PAPERPLICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 bp mRNA illocat
RC2-8FG275-(11199-CII-fill HT0275 Homo sapiens CDNA,
AWSB0638.1 GI:6885297
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EST 06-SEP-2000

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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. A large scale analysis of cDNA in Arabidopsis thattaca: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/cn/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis traliana
Bikaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Mancilophyta: eudicotyledons: core eudicots:
Nosidae: eurosids II: Brassicales: Brassicaccae: Arabidopsis.
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AV551507 Arabidopsis thallana rocts Columbia Arabidopsis thallana
CONA clone R2127f10R 57, MRNA sequence.
AV551507
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/tissue_type="roots"
/note="Vector: pRluescript1: SK-; Site_1: EcoR:; Site_2:
                                                                                                                                                            10 TECATGIGGESTGATECTGGTSGASCAGGATATTGSGATGATGCAGSGGCSSCACAGS
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Kazusa DNA Research Institute
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Bost Local Similarity 56.7%; Pred. No. 6.5;
Matches 112; Conservative 6; Mismatches 108;
                                             Score 37.8; DB 13;
Pred. No. 2;
                                                                                       0; Mismatches 47;
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0; Mismatches 108;
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/Ab_xrof="taxon:3702"
/clone-"R2127f10k"
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Best Local Similarity 58.44
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                                                                                                                                                   Anote-"Organ: head_neck; Vector: p.cl8: Site_1: Smal; Site_2: Smal; A mini-library was made by clonding products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig insultante for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification, were performed under 10w stringency conditions:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM615374 551 bp mRNA linear ESI 25-FEB-2002 17000667146710 A.Gam.ad.cDNA.bloodl Anopheles gambiae cDNA cione 15600449698200 5', mRNA sequence.
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Holt.R.A., Lin,J.-J., Murphy,S.D., Evans.C.A., Kraft.C.L., Gharlab.R.C.lins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 ANTACACACTORCCCGCGGGGGGGGGGGGGCCAGCCGAGTTTAATACCCCTGTGGCGTGATG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            African malaria mosquito.
Anophales gambiao
Ebkaryota: Metazoa. Aithropoda: Hexapoda: Inseta: Prerygota:
Neoptera: Endopterygota: Diptera: Nematocera: Culicoidea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Anophelos gambiae"
Safratos="85F-SI (Reduced susc. to Permethrin - stat.
chromecome)"
/db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                               2.7%; Score 39.6; EB-10; Length 280;
63.8%; Pred. No. 5.33;
tive 0; Mismatches 34; 10dels 0
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/lab_lost="hll0b"
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Fax: 2404534580
Email: HOLLRAdcelera.com
Plate: NUOICO4AAO row: N column: 10
Seg primer: MI3 Reverse.
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/dcv_stage="Adult"
High quality sequence stop: 111.
                     Location/Qualifiers
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Contact: Holt R.A.
Celera Genomics
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Petermination of this BAC-cad sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BUGP). The BGCP is constructing a physical map of the Drosophila. The BGCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BGCP brosophila and melanogaster EAC library was prepared by Kazutoyo Googawa and Aaron Marmoest in Pleater de Jong's Laboratory in the Department of Cancor Genetics at the Rowell Park Cancor Institute in Buffalo. NY. The library is named RPCI-38 and was constructed by partial ECORI digestion of Prosophila DNA provided by the BGCP from the isogenic strain vis. The manual RPCI-38 and was constructed by partial ECORI digestion of Prosophila DNA provided by the BGCP from the isogenic strain vis. The library and how to order individual BAC clones. The entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                               Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
SP 191 91006 EVRY codex - FRANCE (E-mail : seqref<sup>2</sup>genoscope.ns.ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 GAGAATAACATATGAAATGGTTGGAAGAATCCATTATGGCCAAACGCGGTGTTGSTGCCG 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Drosophila melanogaster"
/db_xret="taxon:7227"
/elone="BACROBKId"
/clone=11b="RRC1-98"
/note="end : TEI3"
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llarity 12.2%, Prod. No. 11;
Conservative 173; Mismatches 181;
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Drosophila melanogaster genome survey sequence IET3 end of BAC #
BAC08K14 of RPC1-98 library from Drosophila melanogaster (fruit
                                                                          678 bp mRNA linear ESI 22-FBH-2002 11000687277353 A.Gam.ad.cDNA.blood1 Anopheins gambiae cDNA clone 19600449689205 57, mRNA sequence.
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Match. R.A., Lin, J., Lin, J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
Holf. R.A., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anophelos gambiae EST project
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta: Pterygota:
Neoptera: Endoptertygota; Diptera: Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota: Metazca: Arthropoda: Hexapoda: Insecta: Pteryquia:
Neoptera: Endopteryguta: Diptera: Nematocera: Gulicuidea:
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/strain="RSP-ST (Reduced susc. to Permethran - std.
chromosome)"
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/dev_stage="Adult"
/lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Celera Genomics
45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
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Emall: HOLTRANGCELETA.com
Plate: NU01004AYO row: G column: 15
Scq primer: M13 Keverse.
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/clone="19600449689205"
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                                                                                                                                                                                                                                                     African malaria mosquito.
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Contact: Holt R.A.
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                          RESULT 4
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/dc.xref. has closed malayi Genomic Bac Library 3"
/clone_lib="Brugia malayi Genomic Bac Library 3"
/sex="mixed (me.e and female)"
/Lissue.type="whole parasile"
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/dev_stage="microfilaria" [L2
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Pan troglodytes
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                                                                                                                                   347, UK

Their -44 131 550 6760

Fax: -44 131 550 6760

Email: mark blaxter@ed.ac.uk

Examined from the Erugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by inc Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in Collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Beginburgh, UK.

Seq primer: SP6 (ATTAGGIGACACTATAG)

Class: BAC ends.
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Pan troglodytes DNA, clone: PTB-125G18.F, genomic survey sequence.
AGI17547
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Mammalia, Eutheria, Primates: Catarrhini, Hominidae, Pan,
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Contact: Blaxier Mi
Institute of Coll, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinturgh, EHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 IGTTIGGTATITGTTAATTCTCCCTATTGAAGAACAGATGAAGAAAGIAAAGCTTTCAGTT
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/dlone=lib="Chlom5ch55"
/clone_lib="Chlom5ch56ch56ch5"
/note="Vector: pBluescriptII SK: Site_1: Ec.2: Site_2: XhoI: The CDNA library was constructed from cells cultured in a carbon stress acclimatized condition in which carbon dioxide concentration in the bubbling gas was changed from 5% to 0.04%"
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BMBAC348F06SP6_FSU Brugia malayi Genomic Bar Library i Brugia
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                                                                                                                                                                                                                                                                                                                                                                                  The First Laboratory for Plant Gene kosearch
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0312, Japan
Email: asamizu@kazusa.or.jp, URL.http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 TCAAAGTIGATCTIGAAGTCGCGTGCTTCGTCGAAGTGAGGGGTGGTGTCCAGGATG 146
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( Cases I to 482)

Whitton, C. Daub, G. Ware, C., Quall, N., Hali, N., Barrell, S., Fostes, J., Guiliano, D., Slatko, B. and Blaxen, M.
Genome survey sequences from the human parasitic nematode Bragia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 TIGAAGGIGCTATCAATTCGGAACAGGATATTCCGAGCCAGTIGCTAAAATGCCCTTIC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 TIGACCTIGACGCGAATCACAAACTCCTIGGCSGGGCCSICCTICACGAATCTCAGCTIC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 TCAACCCACAAAACGGACCGATCATGGTCAA13GCGGGGGGAAAAGGTGATGTGCTCCCTG 497
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                                                                                                 1 (bases 1 to 495)
Asamizu.E., Miura.K., Kucho.K., Inoue.Y., Fukuzawa.H., Chyana.K.,
                                                                                                                                                                        Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-SC2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 36; DB 10; Length 495; 45.9%; Pred, No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Chlamydomonas reinhardtii"
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BH767373
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Chlamydomonas reichardtii
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Contact: Erika Asamizu
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Matches 123; Conservative
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/dec_stage="free day old etiolated seedling"
/dec_stage="free day old etiolated seedling"
/dec_stage="free day old etiolated seedling"
/dec_stage="free day old up. 2AP XR, excised phademic palbescript SK: Site_1: EccRI; Site_2: XhoT; Seens were palbescript SK: Site_1: EccRI; Site_2: XhoT; Seens were properature on filter paper with water the dark at zoom temperature on filter paper with water nystation and cetotaxime in covered crystalization diskes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fentor) at the University of California, Riverside. The cDNA closes were in vivo excised to give plusoscript phagemids before cormalization was carried out. The mass excision of phagemid library and normalization were done in HT Nauyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares, Plasmid DNA preparations and DNA sequencing were performed in the CD Anderson lab (all other authors)."
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Erkaryota; Viridipientae; Streptophyta; Enbryophyta; Trembesinytu;
Spermatophyta; Nagnolichhyta; eudicctyledons; core eudinots;
Rosider; eurosids II: Brassicales; Brassicacea; Brassica.
1 (bases 1 to 772)
Town C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgen sequencing of Brassica oleracea
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 GCMAATGAAGCAGCAAGAACTATICCTGGAAGAGAATGGGGGGGAATTGTGACAIAAAG 200
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BOMEL07IF BG_2_5_KB Brassica oleracea genomic close BOMEL77, DNA
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/strain="TO1000DH3"
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  /clone="WHE:101_D03_G05"
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Best Local Similarity 51.2
Matches 82; Conservative
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Fax: 301-838-0208
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Bukaryota, Viidiplantae: Streptophyta: Ethyophyta: Trachesphyta:
Bukaryota, Viidiplantae: Streptophyta: Foales: Poacear; Fooidcae;
Friticeae: Tricicum.
1 (bases I to 6.1)
Anderson 0.2., Chao, S. Chou, D.W., Close, T.J., Feston, R.D., Ban
Ph.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, K., Nguyen, H.T.,
Raussch, C.J., Seaton, C.J., Tong, J.C., and Zhang, B.
The structure and function of the expressed portion of the whose
genomes: Normalized root cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE442556 Wheat elidiated seedling root normalized CDNA WHEIL01_D03_G0528 Wheat elidiated seedling root normalized CDNA library Triticum aest.vum CDNA clone WHEIL01_D02_G05, mRNA
                  1-7-22 Suchiro-chou Tarturi ku, Yokokara, Kanagawa 231 (195), Japan (E-mall)-chimpbes@gsc.riken.go.jp, JKLhhttp://hgp.gsc.riken.go.jp/, Tel.al.45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library FIB Tals RAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1315 TACTCCTICAGCGGAGTGACGGCGGCACAAGAGTIGICACAATGGCGGGGGGAGCAACCAG 1374
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and Chemical Research (RIKEN), Genomic Sciences Center (680);
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Location/Qualifiers
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/cell_cype="lymphoblast"
/clone_lib=PTB Chimpanzee Male BAC Libsary"
/ 186 c 160 g 198 t 3 others
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                                                                                                                                                                                                                                                                                                                                                          1.735
/organism="Pan troglodytes"
/db_xrof="taxon:9598"
/clone="PTE-125G18.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35.6; 1
Pred. No. 13;
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/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                        Vector : pKS145
R.Site 1 : Sacl
R.Site 2 : Sacl.
                                                                                                                                                                                                          Sequencing: -21Ml3
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Contact: Olin Anderson
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                                                                                                                                                            clone tracking errors.
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Best Local Similarity
Matches 62; Conserv
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/lab_host."D810R (amp!cillE_rosistant)"
/lab_host."D810R (amp!cillE_rosistant)"
/lab_host."D810R (amp!cillE_rosistant)
modified poly:inker: Site_l: Not I: Site_l: Ecc RI: St
strand cDNA was primed with a Not I: oligo(dI) primer [5]
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                                                                                                                                                                                                                                                                                                                                  592 GGCCATGCTCAATGATGCGCTGCCAGAAAGGTGCGCATGATTAAACTGGACAGTGAAAA 851
                                                                                                                                                                                                                                                                                                                                                                                      635 GGACTTCCTCGATAAGACGCCGTCATATCAAGCAGAGTTCTTGTAAGAAATCSTAAAAA 577
                                                                                                                                                                                                                                                                                                                                                                                                                                        652 GGTCTACTGGAGGAAAGGGGATACGGTTGGGTATAAACGGGATATTGGGACGTTGAGGGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               576 COTOTAAGTOGAAAAAQGGCCAAAAGAGGCCTAGAAGGCGGCTAACAGCGCACTTALGAT 517
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Sukaryota: Metazoa, Chordata: Craniata: Vertohrata: Buteleostomi;
Mammalia: Butheria: Primates: Catarrhini: Hominidae: Home.
J. (Dases 1 to 268)
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/db_xref="taxon:3712"
/clonc="BOMELG7"
/clonc=lib="Hc_2=3.KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-5 kb sheared
yenomic DNA inserted into pHSS1 using BstXI linkers"
1 165 c 181 g 251 t
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4444 Porest Park Parkway, Box 8501, St. Louis, MO 65108
Tel: 314 286 1800
                                                                                                                                                                                                                         DB 17; Length 772;
                                                                                                                                                                                                                                                                              88; Indels
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/sex="malo"
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High quality sequence stop: 173.
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0; Mismatches
                                                                                                                                                                                                                       2.4%; Score 35.2;
50.0%; Pred. No. 18
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/db_xref+"taxon:9606"
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Email: est@watson.wustl.edu
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Best Local Similarity 50.00
Matches 88, Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eitelecstomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 421)

1 (bases 1 to 421)

1 (bases), Describer, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsous, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meq. J., Irevaskis, E., Chderavood, K., Wohldmanu, P., Watcrston, R., Wilson, R. and Marra, M. Generation and analysis of 286,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 bp mRKA linear EST 01-N3V-1995
gu05f04.rl Soarcs fetal liver spleen lNFLS Homo saplens cDNA slone
mass232927 5', mRNA sequence.
167 CAAGGACTICTTCASCATGAAGCCSGAGTGGGAGAACTTGAACCAGTCCAAGGTGCGGCG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595 CAIGCTCAAIGAICUGCIGCAGAAAGGIGCGCAIGAIIAAACICGACAGGIGAAAGGI 654
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMAGE Consortium (infolimage.linl.gov) for further information.
Insert Length: 1012 Std Error: 0.00
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4444 Portest Park Parkway, Box 8501, St. Louis, MO 53109
701: 314-286 1860
Fax: 514-286 1810
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/db_xref="8DB:2786104"
/db_xref="haxon:9606"
/clonc="TRAGE:232927"
/clonc="TRAGE:232927"
                                                                                                                                                                                                                                                                                                            Query Match 2.4%; Score 35; DB 9; Length 268; Best Local Similarity 50.6%; Pred. No. 9.8; Matches 83; Conservative 6; Mismatches 81; Indels
                                                                                                                                                                                                                                          4 cthers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  655 CTACTGGAGCAAAGGCGATAGGGTTCCCTATAAAGGCCGATATIG 698
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High quality sequence stop: 566.
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Insert Size: 1012
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/tissuc.type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
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/db_xref="GDB:1278736"
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AAGC1557.1 GI:1437022
/sex="male"
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          Hillier, L. Lennon, S., Becker, M., Bonaldo, M.E., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Eavello, A., Gish, W., Hawkins, Chissoe, S., Dietrich, N., DuBuque, T., Eavello, A., Gish, W., Hawkins, M., Huitmau, M., Kucaba, T., Lacy, M., Le, M., Le, M., Marcis, E., Xoore, B., Korris, M., Parsons, J., Prange, C., Ritkin, L., Rohlfing, T., Scielanberg, K., Scarcs, M.B., Tan, F., Thienry Meg, J., Trevackis, E., Underwood, K., Wohlman, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
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IMAGE:363660 3: Similar to WP:K02A2.3 CEC2791 SCMETANIDE-SENSITIVE
NA-K-C1 COTRANSPORTER;; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 CCCACAGGGAGTICTGGGGGGGGAATGGCCGTGCACTTACACCAGGTTGGGGTGTAACC 123
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Mammalia, Eutheria, Primates, Catarrhiof, Hominidae, Home.
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4444 Forest Park Parkway, Box 8501, St. Louis, MC 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                     Query Match
Bost Local Similarity 51.6%; Pred. No. 13;
Matches 80; Conservative 0; Mismatches 75; Indale
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/clone_lib="Soares retina N2b4HR"
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/db_xref-"taxon:9606"
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Ze46d06.sl Scares relina N2D4Hk Homo sapiens cDNA clone
IMAGE:362027 3' Similar to WP:K02A2.3 CE0279! BUMBIANIDE-SENSITIVE
NA-K-01 COTRANSPORTER (contains Alu repetitive element), FRNA
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4444 Forest Park Parkway, Box 8501, St. Louis, MC 53106
Tel: 314 286 1810
Fax: 314 286 1810
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Sources and M.Fatima Bonaldo.
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PCR PKIMETS
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Pahrenkrug, S.C., Preking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, B., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. Design and keele, J.W. and keele, J.W. Besign and use of two pooled tissue corralized cDNA libraries for Grib, blished (2000)
Contact: Smith TPL
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PO Hox 166, Clay Conter, NE 68933-0166, USA
TEL: 402 762 4366
Fext: 402 762 4390
                               /clone="IMAGE:362027"
/clone_lib="Soares retina N254HK"
/sex-"male"
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/db_xref-"taxon:9606"
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4559.050 Million cell updates/sec
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5: /cgn2_6/ptodata/1/ina/ptoTUS_COMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Did.
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US-09-431-573-3
US-08-473-343A-6
CS-09-144-367-7
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US-08-633-770A-3
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US-08-056-260-53
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Abras, John M.
APPLICANT: Abras, John M.
APPLICANT: Grether, Megan E.
APPLICANT: White, Kristin
fille DF INVENTION: Gell Death Genes of Drosophila
TITLE DF INVENTION: Melanogaster and Vertebrate Analogs
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
AUDRESSED: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Iscanigton
STREET: Axington
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MEDIUM TYPE: Floppy disk
COMFUTER: TBM FC compartible
COMFUTER: TBM FC compartible
OPERATING SYSTEM: PG-DOS/NS-DOS
SOFTWARE: PATCATION DATA:
APPLICATION NUMBER: US/C8/123,343A
TILING DATE: 17-SEP-1993
CLASSIFICATION: 800
DRICK APPLICATION DATA:
APPLICATION NUMBER: US US/C04,957
FILING DATA:
APPLICATION NUMBER: US US/C04,957
FILING DATA: IS-AN-1993
ATCHARSAURT INDORWATION:
NAMS: Clanahan, Patricia
                    0.5-0.8-652-643-1

0.5-0.8-99-416-1016

0.5-0.9-522-518-45

0.5-0.9-522-517-7

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48.6%; Pred. No. 0.02;
tive 0; Mismatches 109;
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REGISTRATION NUMBER: 32,227
REGISTRACE/POCKET NUMBER: MIT-5907A
TELEPOMAUNICATION INFORMATION:
TELEPRIONE: 61961-6540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-123-343A-15/c
: Sequence 15, Application US/08123343A
: Patent No. 5593879
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APPLICANT: Steller
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Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli

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PCT-US95-13536-2 PCT-US95-13536-1 US-09-202-893B-3

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APPLICANT: AGAPLIE, MULE
APPLICANT: HC CALL, KIMBERLY
APPLICANT: HC CALL, KIMBERLY
APPLICANT: BERGMANN, ANDREAS
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING AGENTS HAT
TITLE OF INVENTION: LINITRIT NAPK MEDIATED ANTI-ADCHTOLIC SIGNALS
FILLE MEPERENCE: MIT-040.29
CURRENT APPLICATION NUMBER: US/09/431,573
CURRENT APPLICATION NUMBER: US/09/431,573
PRIOR APPLICATION NUMBER: G6/106,108
PRIOR APPLICATION NUMBER: G6/106,108
PRIOR FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      999 GSAGCTCTTCTTCTTCCGGGGGGGGGATGCGTCCATGAACTCCTGCAGACGCTCCGGCC
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TITLE OF INVENTION: INHIBIT MAPK MEDIATED ANTI-APOPTOTIC SIGNALS
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48.6%; Pred. No. 0.035;
tive 0; Mismatches 109; Indels
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Local Similarity 48.6%; Pred. No. 0.035;
nes 103; Conservative 6; Mismatches 109;
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              FILE REFERENCE: MIT-04019
CURRENT APPLICATION NUMBER: US/09/431,573
CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/106,108
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 5
SOFIWARE: Patentin Ver: 2.0
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Patent No. 6235524
                                                                                                                                                                                                                                                ORGANISM: Drosophila melanogaster
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SOFTWARE: PatentIn Ver. 2.0
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Matches 103; Conservative
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                                                                                                                                                                                SEQ ID NO 2
                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
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                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                     LENGTE:
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                                                                                                                                                                                                                               GAAGGTGCTATCAATTCGGAACAGGATATTCCGAGCTGCTAAAAAATGCCCTFICTC 439
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                     ACACCCGTCCTCACCATCGAACCCGGTGACCGGATTATTGTCGACACTCGAGATGTTTT 379
                                               GAAGGISCTATCAATICGGAACAGGAIATICCGAGCCAGTIGCTAAAAATGGGCTTTGTC 439
                                                                                                                                                     274 SGAGCICITCITCCGGGGGGGGATGCGTCCATTSAACTCCTGCAGACGTCCGGGGC 215
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BADELEAUT: STELLER: HERMAN
APPLICANT: AGAPITE, JULIE
APPLICANT: Mc CALL, KINBERLY
APPLICANT: HERGMANN, ANDREAS
APPLICANT: HERGMANN, ANDREAS
APPLICANT: HERGMANN, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: STELLER, HERMAN
APPLICANT: STELLER, HERMAN
APPLICANT: MG CALL, KIMBERLY
APPLICANT: MG CALL, KIMBERLY
APPLICANT: MG CALL, KIMBERLY
APPLICANT: BERGHANN, ANDREAS
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING AGENTS THAT
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING AGENTS THAT
CURRENT APPLICATION NUMBER: US/09/431,573
CURRENT FILLEN DATE: 1999-10-29
PRIOR FILING DATE: 1998-10-29
NUMBER C SCG ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.6%; Score 37.6; DB 4: Length 1233; 46.6%; Pred. No. 0.035;
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Patent No. 6235524
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09431573
Patent No. 6235524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA CROSOPhila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0 SEO 1D No.1 LENGTH: 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103: Conservative
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US-09-431-573-1/c
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Matches
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Gaps

939 OGCCGIAAAGTTGICGTAGCGAICGCCAAACICGICCCCAAGTGGCCTCAIGATCGCTCTG 880

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APPLICATION NUMBER: US/08/473,553A FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MANCHY TYPE: Floppy disk
CMENTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/38473553A Patent No. 5859338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     2.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 781-198
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
SIATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 57.5
hes 61; Conservative
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (0)...(0) CS-09-144-367-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Other
 RESULT 6
US-09-144-367-7/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38-08-473-553A-1
                                                                                                                                                                                                                                                                       SEQ ID NO 7
LENGTH: 429
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steller Hermann
APPLICANT: Abrams, John M.
APPLICANT: Grether, Megan E.
APPLICANT: White, Kristi:
TILE OF INVENTION: Cell Death Genes of Drosophila
TILE OF INVENTION: Melanogaster and Vertebrate Analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PC-DOS/MS-LOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPRICATION NUMBER: US/08/123,343A
FILING DATE: 17-SEP-1993
CLASSIFICATION: 800
PRIOR APPLICATION -
                                                                                                                                                                                                                                                                                                                      E: Hamilton, Brook, Smith & Reynolds, F.C.
Two Militia Drive
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SOC TATAICGAATCCATGTTGCCCCGCGCGTTGA SSI
                    879 GTACTCGCGCTCAICCTCGCCCGGTCGAGGTCA 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5907A
TELECOMMUNICATION: 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,957
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                          Sequence 6, Application US/08123343A
Patent No. 5593879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.6%;
Matches 103; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 61861-9540
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 021/3
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3900 base pairs
                                                                                                                                                                                                                                                                                          16
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                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
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                                                                                        RESULT 5
US-08-123-443A-6/C
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ZIP: 02173
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1164 ACAAAAACCIGTTAGTTAGTAGGAATAACTAACCGGTGAACAITACCCGGAIGTAGATG 1223
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APPLICANT: Clark, Steven E.
APPLICANT: Clark Steven E.
TITLE CP. INVENTION: Flant Clavatal Nucleic Acids,
TITLE CP. INVENTION: Transformed Plants, and Proteins
NÜMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
ADDRESSEE: FICHT, Hobbach, Test, Albritton & Herbert,
STREET: Four Embarcadoro Center, Suite 3496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWAKE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35.2; DB 4;
Pred. No. 0.12;
1; Mismatches 44;
Sequence 7, Application US/00144367
Patent No. 6432639
GRNERAL INCRARATION
GRNERAL INCRARATION
GRNERAL INCRARATION
GRNERAL INCRARATION
TITLE OF INVENTION GRNCTPFING OF HUMAN CYP3A4
FILE REPERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: 05/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR FILING DATE: 1997-09-10
NUMBER POL SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
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ER: A-60886/RFT/RMS
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C: Gaps

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APELICANT: Krajh, Karsten
APELICANT: Christenaen, Tove
APELICANT: Marcussen, Tove
APELICANT: Marcussen, Tove
TITLE OF INVENTION: ALPHA-1.4-GLUCAN LYASE PROM A FUNCIN, TIS
TITLE OF INVENTION: PUR-PICATION GENE CLONING AND EXPRESSION IN MICHOPORGANISMS
COMPRER OF SEQUENCES: 12
COMPRER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 CCGGGCGTAAACCGGTAACGCATCACCTGACGGAAGAATGCAAAAAGAGTTTCATTACA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 CCATTGGCCCTTATTCCACACCCGTCCTGACCATCGAACCCGGTGACCGGATTATTGTCG 362
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,770A
FILING DAIE: July 8, 1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION COT-15-1994
AITCHNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               83;
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 83; Conservative 0; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Knobbe, Martens, Clson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFFRENCE/DOCKET NUMBER: 34,115
REFFRENCE/DOCKET NUMBER: DYCU5.001APC
TELECOMMONICATION INFORMATION:
TELECHORE: 714-756.0404
TELERAX: 71,-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-533-770A-11/c
7 Secrence 11, Application US/08633770A
7 Patent No. 5508760
                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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SROUBINGE CHARACIERISTICS:
LENGTH: 4726 base pairs
TYPE: uncleic acid
STRANDEDNESS: SINGLE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGIH: 3201 base pairs
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bojsen, Kirster
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REGISTRATION NUMBER: 3
                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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MOLECULE TYPE:
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APPLICANT:
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APPLICANT: Marcussen, Jan
TITLE OF INVENTION: ALPHA-1.4-GLUCAN LYASE FROM A FUNCUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICHORDANISMS
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 111 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 | 117 
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/633,770A
FILLIG DATE: July 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FP94/03398
FILLING DATE: OCT-15-1994
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STRWET: 620 Newport Center Drive 16th Floor
Cliy: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.4%; Score 34.2; Silarity 50.3%; Pred. No. 1.2; Conservative 0; Mismatches
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REFERENCE/DOCKET NUMBER: DYCU6.COLANCELECOMMONICATION INFORMATION:
TELEPHONE: 714-760-3404
TELEPAX: 714-760-3404
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Patent No. 5908760
                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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GENERAL INFORMATION:
APPLICANT: BOJSEO, Kirsten
APPLICANT: Yu, Shukun
APPLICANT: Kiragh, Karsten
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                              INFORMATION FOR SEQ 1D NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
TYPE: nucleic acid
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REGISTRATION NUMBER: 34
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MEDIUM TYPE: Diskette
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TELEX:
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5117..5467
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Matches 84; Conserv
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TOPOLOGY: ur
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LOCATION:
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LOCATION:
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Rest Local Similarity
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US-08-056-200-93
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                             Leagth 4726;
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OPERATING SYSTEM: PC-CCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Best Local Similarity 3.6%; Pred. No. 4.2;
Matches 13; Conservative 193; Mismatches 160;
                                                            83;
                              DB 33
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
ACPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEGUENCES: 52
                                                            0; Mismatches
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                             Score 33.2;
Pred. No. 2.4
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1800 Diagonal Road, Suite 500
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FIGING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                             RESULT 10
US-08-232-463-14/C
Sequence 14, Application US/08232463
Parent No. 5670367
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                             2.3%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                           Query Match
Best Local Similarity 50.09
Matches 83; Conservative
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STRANDEDNESS: single
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ADDRESSEE: Foley & L
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US-08-633-770A-11
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212 REPRESERVER FRANKER FRANKER FRANKER FRANKER FRANKER FRANKER 1153
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1111 AGTGCGGCTGGGCAACATGGTCGACCCCAAATACACGGTTGGCGGGATGCTGAACAAAA 1170
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                                                                                                                                                                                                                                                                                                                   1171 CCTGTTAGTTTAGTAGSAATAACTAACCGGTGAACATTACCCGGATGTAGATCGSGGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 ANATGCCCTTTCTCAACCCACAAAACGGACCGATCATGGTCAATGGCCCGGGAGAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garis
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IIILE OF INVENTION: Retroviral hybrid vectors pseudotyped with ECMV
FILE REFERENCE: P50489
CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT FILING DATE: 1999-35-11
FARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER APPLICATION NUMBER: DE 198 56 463
NUMBER OF SEO ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
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54.1%; Pred. No. 3.5;
tive 6; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Lymphocytic choriomeningitis virus 29-309-572-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 93, Application US/08056200 Patent No. 5616500 GENERAL INFORMATION:
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Sequence 3, Application US/09309572
Patent No. 6440730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee, Scung-Chul
Kim, In-Gyu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Chung, Soo-II.
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Tricholyalin and Transglutaminasc-3 and
TITLE OF INVENTION: Mehods of Using Same
COMPRENCE: 117
CORRESPONDENCE: 117
                                                                                                                ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Conter Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                     SOFTWARE: Pateuttn Rolease #1.6, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/GB/BUG, 644
FILING DATE: 14-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: PEOLICK, Michael F.
REGISTRATION NUMBER: 86,799
REPERENCE/DOCKET NUMBER: 81,799
RELECOMMUNICATION INFORMATION:
TELEPAR: (714) 760-0404
TELEPAR: (714) 760-052
INPORMATION FOR SEQ 10 NO: 93: SEQUENCE CHARACTERISTICS:
LENGTH: 19551 base pairs
TYPE: 1001-60-053
STRANHERNESS: SINGLE
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APPLICATION NUMBER: US 08/056,250
FILIND DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATINS SYSTEM: PC-TOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1507..1644
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1645..2511
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2512..6070
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CLASSIFICATION: 424
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MOLECODE TYPE: CDNA
HYPOTHETICAL: NO
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2.
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21P: 92660
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US-08-374-686-4/C
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LOCATION:
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LOCATION:
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LOCATION:
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FEATURE:
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                APPLICANT: Park, Sang-Chul
TITE OF INVENTION: Trichchyalin and Transglutaminase-3 and
TITE OF INVENTION: Trichchyalin and Transglutaminase-3 and
TITE OF INVENTION: Webods of Using Same
WUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
CITY: Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
SIMPLE: CA
SINTE: CA
SINTE: U.S.A.
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Indels
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                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Sciedae #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/GH/C56.200
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                               AJTORNEY/AGENT INFORMATION:
NAME: FEGITICK, MICHAEL F.
REGISTRATION NUMBER: 36,799
REFERENCE/COCKET NUMBER: NIMCS4.001A
JELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
THEFRATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5958752
GENERAL INFORMATION:
APPLICANT: Steinert, Peter M.
APPLICANT: Lec. Scung-Chul
APPLICANT: Kim, In-Gyu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 9551 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 81; Conservative
  Chung, Soc-Il
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2512..8070
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1645..2511
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: LOCATION:
:US-08-056-200-93
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US-08-800-644-93
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3064 CGAGAGCGCCAAGACAGAGTGTTCCAGGAGGAAGAAGAAGAAGAGTGGAGGAAGCGCGAG 3123
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                                                                                                                                                                      3 CGGGAACICCATGIGGCCGIGATCCIGGTCGAGGAGATATTGCGAISATCCASCGGGCC 62
Query Match 2.2%; Score 32.4; DB 2; Length 9551; Best Local Similarity 50.0%; Pred. No. 6.7; Matches 81; Conservative C; Mismatches 81; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3184 CTCCAGSAGGAAGAAGAGCTACGGAAGCTGGAGCGGCAA 3225
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Patent No. 5616474
GENERAL INFORMATION:
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Caps
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Best Local Similarity 63.6%; Pred. No. 2.2;
Matches 49; Conservative U; Mismatches 28; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bolotin, Monique
APPLICANT: Bolotin, Monique
APPLICANT: Menart, Sandrine
TITLE OF INVENTION: R. lactis Transaldolase Gene Fromoter
TITLE OF INVENTION: and Use Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer inc.
STREET: 500 Arcola Ed. 3043
                APPLICANT: Menart, Sandrine
TITLE OF INVENTION: K. Jactis Transaldoluse Denn Promotor
TITLE OF INVENTION: and Use Thereof
WINTER OF SEQUENCES: 5
CURRESPONDENCE ADDRESS:
ADGRESSORE: Rhone-Powlenc Rorer Inc.
STREET: 500 Arcola Rd. 3C43
                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-FDS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,686
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NONTA:
APPLICATION NUNBER: WO PCT/FR93/00771
FILING DATE: 28-JUL-1993
PRIOR APPLICATION NUNBER: FR 92/09432
FILING DATE: 30-JUL-1992
ATTORIEX/ASDRY INFORMATION:
NAME: Smith, Julie K:
REGISTRATION NUMBER: 36,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE DOOR TIME TO ST92048-US TELECOMMUNICATION INPORMATION:
TELEPHONE: (610)454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08374686
Patent No. 5616474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1220 SATCGGGGTAATGTGTA 1236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELLEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
APPLICANT: Bolotin, Monique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 1226 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Collegeville
                                                                                                                                                        SIREFT: 500 Arcola CITY: Collegeville
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                                                                                                                                                                                                                           USA
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                            19002
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                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-374-686-4
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1160 CIGAACAAAAACCIGTTAGTITAGTAGGAATAACTAACCGGTGAACATTACCCGGATGTA 1219
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                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/374,686
                                                                                                                                                                         PRICE APPLICATION: 435
PRICE APPLICATION DATA:
APPLICATION DATA: WC PCT/FR93/00771
FILING DATE: 28-JUL-1993
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: FF 92/09432
FILING DATE: 40-JUL-1992
ATTORNEY/AGENI TWORMATION:
NAME: SMITCH JOJIE K.
REGISTARTION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NORBER: ST92048-US TELECOMMUNICATION INFORMATION: TELEPHONE: (610)454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scarch completed: July 6, 2003, 06:42:25
COMPUTER PEADABLE FORM:
MEDIUM TYPE: FLORDY SISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACIERISTICS:
LENGTH: 1349 base pairs
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Matches 49, Conservative
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BDNESS: single
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ANTI-SENSE: NO
ORIGINAL SOURCE:
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen 15d.

OM nucleic - nucleic search, using sw model

July 6, 2003, 02:01:46; Search time 3753 Seconds (without alignments) 1182.053 Million cell updates/sec Run on:

US-10-086-082-1 1442

1 eccyggaactecatgtggee.....aatgeaatteatttggatee 1442 Title: Perfect score: Sequence:

IDENTITY_NUC Gapext 1.0 Scoring table:

4109280 Total number of hits satisfying chosen parameters: 2054640 seqs, 1455;402878 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000060000

GenEmbl:• Database :

9b_ba: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

1442 bp Sequence 1 trom Patent WO980255: A69475: A69475:1 GI:476023: RESULT 1 A69475 CCOUST CCESTON ACCESSION VERSION KEYWORDS SOURCE ORGANISM

PAT 06-MAY-1999

linear

DNA

Klebsiella oxytoca.

Klebsiella oxytoca
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Klebsiella
. (bases 1 to 1442)
Bovenberg, R.A., Van, D.L., Kerkman, R. and Nieboer, M.
IMPROVED PROCESS FOR THE PRODUCTION OF ADIPOYL CEPHALOSPORINS
Patent: WO 9802551-A 1 22-JAN-1998;

REFERENCE AUTHORS TITLE JOURNAL

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Brieden,W., Naughton,A.,
Zimmermann,T.
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                                  TGAACATTACCCGGGTGTAGATCGGGGTAATGTGTAAGGTTCAAACAATCGCTATTTTAA
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                                                                                                      /protein_id~"CAB42722.1"
/db_xref="G1:4808108"
           /organism="Klebsiella
/strain="PRS1"
/isolate="PRS1"
                                              /db_xref="taxon:571"
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/transl_table-11
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/protein_id="BAB72558.1"
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SAIAFVWGGAFFADTSAMADNSTYLIATSDATDSLRNKSKEFIRDTKDNVKDAARINA
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FVYTPKHFPLTNSINEYRDQLGKRPPLATMELIWCPYAGDAHVIAGYVHPPTEGMFQV
ALELRGVSKFTLVKGLEGSCDLRDRTAIISLSSASPELERVFLSTHEYGFTTKNVPL
GSTEELLTQYQDVLAGKSCELQQTALWNGGFYLWRSGICADMRSGIAKAEELLNSGLV
AAKLOELIQVVNSVTENLLSIT"
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YQDIOTVLKTDVMKGYRGNLFFPNORYTRABLAIFAQAYGYFOFSDDVVNELLAPYP
DANSIPNWARRAIATVITEGFINTDAQNNITPLRPMTRGDMAYLL,SKYLQRQOKQPDT
PVVPTTTDSPQLP"
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                                                                                                                                                      /translation="MKQFSSEVEEKSVVEVDWADRWQVYQRLQELEIPCWCEANGPLK
VELVTPWTVVQLWSVWRQFTSSRQDLIYSLEINWQSRYPYS"
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GLGVVELTLGLYQTLDLDRDKVIWDVGHQAYPHKLITGRYSDFHTLRQKDGIAGYLKR
GENKFDHFGAGHASTSISAALGMALARDMNGEKFKAVAVIGDGALTGGMALEAINHAG
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VHVATIKGKGYELAEKDQVGYHAQTPFNLTTGKAIPSNKPKPPAYAKVFSHTLVKLAE
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STFI,QRAYDGITHDVCIQNLPVFFCLDRAGIVGSDGPTHQGMYDIAYLRCIPNIVMA
FKDFAEMQRMVYTGIBHTTGPIAMRFPRGNGYGVPLMEEGWEPLEIGKGEILRNGDDV
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/db_xref-"GI:17129945"
                                                       /protein_id="BAB72555.1"
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/gene-"all0601"
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/note="ORF_ID:alr0599"
/codcn_start=1
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DEISRITAAALLAKKGGLEAFKALASALKNEPPROVBVEDKAROLLASIKLDGAFGGLVE
BLADKHAYVBRAVVONLAK IKTLASYKAVKOVVKDGDASYYVESAACLALGATAAIN
DDKSKEFKAIKLLQSVLEERRGWNEVVRSGAIGGLAELKTSEAALDEI. IHTTKIGVPY
PLEAAAIRAGGISPQQSPVNLERIIARLGEGESKENFPLTIARAVVAALGQMETPKAMG
VLRSLAADQTADGRVRRFAEEELANVQKNIGTDNALRKIRFFFGOLKGGNOELKSRIEN
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                                                                                Submitted (02-MAZ. 2001) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; Yana 152-3. Kisaarzu, Chiba 292-0812, Japan 153-3. Kisaarzu, Chiba 292-0812, Japan 153-3. Kisaarzusa.or.jp/cyanobase/, URL:http://www.kazusa.or.jp/cyanobase/, Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)

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similar to cytochrome d oxidase chain I"
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/qene="as10597"
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/gene="all0596'
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                                                        BCT 12-JUN-2002
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                                                                                                                                                                                                                                                                                                          Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J., Heidelberg, J.F., Aliey, M.R.K., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J. Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Shepiro, L., Venter, J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                       Caulobacter crescentus CB15
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
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Proc. Natl, Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
                                                     AE005929 13698 bp DNA linear
Caulobacter crescentus CB15 section 255 of 359 of
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Caulobacter crescentus CB15
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//db_xref="GI:17129948"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               738 CACTGACGCCAGACAATCACGGCGGGAAIATGGATGTGCCGGAIAIAGGACCAGGGAGIA 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      658 STCAGGGTGATGGTGAGATTTGCGGGACCGCAGTAGAGTTTGCCCTCAATCACCACCATCA 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTCGATTTGATCAAGAACTGGCAGCTTTCCTGGCCACGAATGGGAGAATGGCGGAAATA 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  798 TIACCIAICIGCGGIACGISCGCCIGGAGGCGGCCTGTTATIGGIGATGCCCATGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          putative transcriptional regulator'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(10861. .11166)
/gene="all0663"
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.10618)
                                                complement(9580, .10518)
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Pred. No.
                                                                                                /note-"ORF_ID:all0602
ntcB gene product."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"ORF_ID:a110503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="all0604"
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hypothetical protein"
complement (9680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene-"all0603"
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                                                                                                                                                         /codon_start-1
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                          /qene="ntcB
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Best Local Similarity 47.6
Matches 218; Conservative
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/gene-"CC2613"

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/LTGESTALLON="MADSAAAPIKAPPQGVHAALPHDSAARHVAGSAVYIDDMPEPA
GELHVARGESBRAHARTIRANDLSAVRARAPOVYISAEDIYOENDVSYPYIHDDKLFAD
GELHVARGESBRAHARTIRANDLSAVRARAPOVYISAEDIYOENDVSYPYIHDDKLFAD
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WYWTGKRHDFFALYVUGFDGEGRIFGLISLAISSRCGATTDLSPAINDRAFKARPDRDED
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FMKRLRDDGFSEAVLTRLTCPIGLPHIKSKAPEVIAVSAADLLMROEAARIRNDEMS
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SEVLLDTLIGEMKYTRADILHDVGKSLNPALDLGGIEGGFIQGMGWLTTEELVFDAQG
RLRTHAPSTYKIPTGGDRPAQLDVRLWKAGRNVEATVIRSKAVGEPPLMLAISVHSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSGLTTHILDQASGKPAAGVGVRVSRRDGEQTQMLAELRTDADG
RARLVAGEDLAVGGYRLEFAIGDHFKASGLPVSDPPFLDVVVIDFAVSNLDQHWHVPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene "CC2619"
/gene "This region contains an authentic frame shift and
is not the result of a sequencing artifact; identified by
match to protein family HMM; xanthine dehydrogenase,
putative, authentic frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"identified by match to PFAM protein family HMM
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/product="xanthine dehydrogenase, C-terminal subumit"
/product="xanthine dehydrogenase, C-terminal subumit"
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/note-"identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THAVASVGDHKVFPDLDAPATPEAILMACEDVRRRARDV"
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/db_xref="G1:13424192"
/translation_id=10.1
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57.6%; Pred. No. 1.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                           /gene-"CC2618"
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3376. 4347
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LLALGRVADALEARDEVT_DNAQARAAAFCLTAFEGGELHHEDLARRAMDYDPAVRD
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VPVSYRKNIGAFIGTSYVGLPVLAAPVNRPGQLPIGVQIIAPPWREDLAFAAALR_C
RAGVVAAHPPMGAL*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKPGNVTPVAEANIWNDPEAADOVFTAPWNI,TAVSLOVTTQVVASPDYNDALAAGGSD
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VAAGLVPLTLGSDINGSIRIPAGLCGVFGLKPTYGRLSRQGVFPFVESLDHVGFPRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /::dns__tdDie=.i
/product="inosine-uridine_preferring_nucleoside_hydrolase"
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                       /gene="CC2613"
/note-"identified by match to PFAM protein family HMM
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                                                                                                                                      /transl_table=11
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PPDLETRIAILRKKAKAFULDIPNEVMLYIANQIDTNIRELEGALIRVVAYSSLINQD
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                    Nakasone, K., Masui, N., Takaki, Y., Sasaki, R., Maeno, G., Sakiyama, T., Hirama, C., Fuji, F. and Takami, H. Characterization and comparative study of the rrn operons of aikaliphilic Bacillus halodurans C-125 Extremophiles 4 (4), 209-214 (2000)
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VTTIRSGSSVFNLNGLDPDEYPRLPVLEEDHVFRLPQKILKDIIRQTVFAVSTQETRP
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BNEBLLDIVYDFNQTLFKIKNMLFFSRELEGKYPTKNMIPRERATSFAVHTKAFIQT
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KNVIDALKVVDSESIHIAFTGAMSPFVLSPTDHDQSLHLFSPVRIY*
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ApnefardwlekhydelisetiddltgvrlypkfviptsqldepfveqelkkpmkQpp
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URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html,
Tel:81-468-67-3895, Fax:81-468-66-6364)
Location/Qualifiers
                                                                                                                                                                                                                                                             Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleis Acids Res. 28 (21), 4317-4331 (2000)
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Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and
Horikoshi,K.
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Takami,H. and Takaki,Y.
Direct Submission
Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and
Technology Center, Deep-sea Microorganisms Research Group; 2-15
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
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/product="initiation of chromosome replication"
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/protein_id-"BAB03721.1"
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to Bacillus halodurans
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Takaki.Y., Nakasone,K., Sakiyama,T., Macno,G.,
Takami.H., Takaki.Y., Fuji.F. and Masui.N.
Genetic analysis of the chromosome of alkaliphilic Bacillus
halodurans G-i25
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Replication origin region of the chromosome of alkaliphilis
Bacillus halodurans C-125
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Takami,H., Takaki,Y., Nakasone,K., Hirama,C., Inose,A. and
Horikoshi,K.
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Bacillus halodurans genomic DNA, section 1/14.
AP001507 BA000004
AP001507.1 GI:10172612
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Extremophiles 3 (1), 21-28 (1999)
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19-284: Springer-Verlag (1999)
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Awayez,M.J., Chan-Weiher,C.C., Clausen,I.G., Curtis,B.A., De
Moors,A., Erauso,G., Fletcher,C., Gordon,P.M., Heikamp-De Jong,I.,
Jofffise,A.C., Kozera,C.J., Medina,N., Peng,X., Thi-Noc,H.P.,
Reder,P., Schenk,M.E., Theriault,C., Tolstrup,N., Charlebois,R.L.,
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The complete genome of the cremarchaeon Sulfolobus solfatarious P2
Proc. Natl. Acad. Sci. U.S.A. 98 (14), 7835-7840 (2001)
                       GUGGGAATATGGA7GTGCCGGATATAGGACCAGGGAGTATTACCTATCTGCCGGTACGTG 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota; Thermoprotei; Sultolobales; Sulfolobaceae;
Sulfolobus.
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Direct Submission

Submitted (24-APR-2001) Europe/Canada joint project: Copenhagen University, Denmark; University Paris Sud, France: Wageningen Oniversity, The Netherlands; Institute for Marine Biosciences 6
                                                                                                                                                                                      879 GCGGGACCGCAGTAGAGTTTGCCTCAATCACCACCATCAAAGTCGATTTGATCAAGAACT
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Location/Qualifiers
1. .10485
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FEGGYKTKLGNSEARTITDSLFTEHFSFFLIEIPOVARKLVNKGLMASRAŁBAAKKAR
ELTRRKSALEVSLPGKLADGSSRDSJSEJYTVEGDSAGGSNKOGNDRIFUGALIFUG
GKILNVEKARIDKILDANETRALITALGTGTODPEDIEKARYKIIINTGADVDGAH
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Pred. No. 4.2e-06;
0; Mismatches 281; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="BH0005
unknown conserved protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /EC_cumber-"5.99.1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="BH0005"
/788. cor
                                                                                                                                                                                 /note-"BH0004"
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5130, 7043
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                                                                                                                  /gene="recF"
3662. .4777
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/gene="recF"
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Best Local Similarity 44.9
Matches 229; Conservative
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LSVADRARNITALAASYKLLGKEGYLINSTTRTFRQEVFAKINTIAAQLAMQOIQPH
YNLFELPNNEEKINLDGNTAAAIGKIYGGLEFQSYYPITPASDESVFIEAHQTVFTVD
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LNIAQKYOTPVIHLVDKALANSYSIIPKKTLGMENIRIEKGRIVINNYPELKRFEII
EGGISPFAPLGTARVHYIGDEHDEVGFIAEASERIKEMATADKEIPESR
VNYGNTDSKVATTORGYILDAMEELENEGIRPKLIOTRMISPFPKNLMKKLIN
GKEFIIDSSNYFGQAGEVIKINTGIFPTHYIKWNGRPMMRDEVKEGIRAVVOKGER
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DQLGIGVGHFVSAGRRNVDLTVIVHNNGVGLTKGQASPTLKLGVKTKSLPKPNINSD
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PKKiDILIVKQTDRSKIIEAVKMYKLFECNNITKEECLVKVLNRVFFYCKTCRFT"
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                                                                                                                                        complement(6317, .6799)
/qene="SS02813"
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complement(6923. .7225)
                                                                                                                                                                                            complement(6317, .6799)
/gene="SSO2813"
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/gene="SSO2815"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"Medium-chain-tatty-acid--coa ligase (alkk-s)"
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IDRLKDLIKSGGEWISSVDLENAIMSYFKVLEAVVVGVKDERMGERPTALVVKRFGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"Transposase ISC13i6"
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/cranslation-"MPTLGFRFRAYIDEUTLRAIKAGLKLACKIYNTHRWADTYFYOR
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PHKYYSLVYTOSUM TIAPRETRKOSKNIKKKI, TIKINSINGTRKVY VHHEPEIDKYK
PHVYXXLIRSER IV TEVVBGYTEFPKLENTGKVVATDVOVBKILIVTEGBEYEPBLIRELE
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LMTGAKLVLPGPRPKAEDIVKLIKEFKVTVGVGAPTVWJDVVNYVERENVDLHJKVVV
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ARGGYVKNDI.SI.SDRVFVCPNGGWIADADYNASLNILKGAGSERSJVPVELARFI.PVPA
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2640. 3596
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/product="Hydrolase, acetamydase/formamidase related,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Hypothetical protein"
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/note="Energy Metabolism"
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                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Lipid metabolism"
/codon_start-1
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/transl_table=11
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3693. .4928
                                                                                                                                                                                                                                                                                         /note="5502808"
1073. .2596
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/gene="SSO2810"
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/gene="SSC281:"
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                                                                                                                                                                                                                                                      1073. .2596
/gene="alkK-3"
                                                                                                                                                                                                                                                                                                                                                            /yene-"alkK-3"
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SIAGE V SPORULATION PROTEIN D (SPORULATION SPECIFIC PRESCILLED BURGILLINE BINDING PROTEIN 941121233919111845970 penticillin-binding protein (spore cortex) spown - Bacillus subtilis 911580936|emb|CAA81085.1| (225865) SpowD [Bacillus subtilis] 9112533888|emb|CAB813390.1| (299111) penticillin-binding protein [Bacillus subtilis], score 396, E-value 1.00E-109*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGVDGYGLYGLEYSLDRYLSGYPGREISLVDRRGHKYGIPSKYYKPRGGEDVYLTYDS
VIQAYTERAIKKAYERYKPEDGITAIVMNPKTGEILAMANLPDFDPNDPQKVPSGEYW
ANPAYSSIYEGCSYFKYITAAALDSAVVTPEEDCPPDGYYEVSGKKIRSWYLGNIT
FSQAIEKSSDTVFIOVAERLGJDFYRYTOPGFFGAPTGIELPGEASGMILPKDKYY
VDFAJNSFGGGIAVPTDMITAFSAVINGGDMYPHIVKIKSEGKIVKEFKROVYKO
VISKETSDTLRYILEKTVTEGTGQLAQVPGYRVGGKTGTTENYQKGKYTASFAGFAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product.-'Sugar-binding periplasmic proteins/domains"
/protein__id="AAM25097_1"
/db_xref="GI:20516927"
/db_xref=to:-"Sugar-binding periplasmic proteins/domains"
/db_xref=to:-"FORTAMENTED THE TELETANMENT THE TOTAMENT THE TOTAMENT THE TOTAMENT THE TOTAMENT THE TOTAMENT THE TOTAMENT 
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YNTAALVESSYKLAELSKULKKKGKLEFDVAPFTGESGIPLTISPKYYGYGIKKDK
DLKKLEMEYRIJKFYVQLCEGVLKLGYVPTKKGIEIGEEKMKKIFEAVKYTELPPLWD
KWEKVNNLVIERVKEGIKEGKSAYEVIFGIKKEVGE"
                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id-"aaM25096.1"

Lab.xref = 'G1:20516826"

/tab.xletion="WKSLKLFFFFFFFILESILIGRLVWIOVVNAEKLSLAVER

OTTADIIIRPORGNIYDVNGNILACNVPAADVYASPKYIKDPEKASEELSKYLSISKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALFKVLSKKDLEWTVLERFVPMEKALSIKKLNIPGIYVEDTSMRNYPNGSMLSQVLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"pitative rho-independent transcription terminator"
complement(3190. .3855)
/gene-"MipB"
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                                                                                                                                                                                                                                                                                                       /transl_table*11
/product="Cell division protein FtsI/penicillin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Pfam match to entry Transpeptidase, Penicillin
binding protein transpeptidase domain, score 410.9,
E-value 1.20E-119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Best Blastp hit - gi|12722179|qb|AAK03846.1;
(AE005213) unknown [Pasteurella multocida], score 67.
E-value 3.00E-10"
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/product="Transaidolase"
/protein_id="AAM25098.1"
/db_xref="G1:20516928"
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/gene="Fts14"
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Thermoangerobacter tengcongensis strain MH4T, section 159 of 244 or
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Submitted (07-00T-2061) Institute of Microbiology, Chinese Academy of Sciences, Beijing 100080, China
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                                                                                                                                                                                                                                                                         3164 AGGCACGAAGTIATATCICCCAGTGTTIGIGAATGGAGCACTACTTICCATAGGTGAIAC 3223
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Bao,Q., Tian,Y., Li,W., Xu,Z., Xuan,Z., Hu,S., Dong,W., Yang,J.,
Chen,Y., Xue,Y., Xu,Y., Lai,X., Huang,L., Dong,X., Ma,Y., Ling,I.,
Tan,H., Chen,R., Wang,J., Yu,J. and Yang,H.
A Complete Sequence of the T. tengcongensis Genome
Genome Res. 12 (5), 669-760 (2002)
                                                                                                                                                                                                                           730 AATCAATTCACTGACGCCAGACAATCACGGCGGGAATATGGATGTGCCGGATATAGGACC 789
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Back, Wars, Warg, Chen, Y., Warg, C., Yu, J. and Yang, E., Direct Submission
Submitted (07-ccr-2001) Beljing Genomics Institute/Genomics and Bloinformatics Center, Institute of Genetics and Development, Chinese Academy of Sciences, Beljing Airport Industrial Sche Be, Beljing 101300, China 3 (bases 1 to 7983)
Liw., Xuan, Z., Yang, J., Ling, L. and Chen, R.
Direct Submission
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Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                    Length 10485;

    7983
/organism="Thermoanaerobacter tengcongensis"

                                                                            4.1%; Score 59.8; JB 1;
55.6%; Pred. No. 3.4e-06;
iive 0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3284 IACAGTGAAGGTTAGATTAAAAA 3310
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/gene="Fts14"
155. .1816
/gene="Fts14"
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AEC13142 AEC08591
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Pred. No. 5.6e-06;
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/note-"TTE1922"
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LMFLCHR36_25
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CMFLCHR36_23
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LMFLCHR36_27
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/db_
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NSLNFDLENIIKNFPHISFIIISKTTPEPVYDIADRIYILHEGKIKKS.1AKQDYSSLEK
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LTLFLCAVGLSVAGTSMAFTISYTLFFGLLFGLYISFKRSESILLIFLLFLHELFSF
LVAKRFEKEKMAFIY*
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ITASVAHFIHVIFAAKIGAHTAVPYKVIMQMIKHELTDIGISHFKHWKKAGIKI
COMPIEMENI(3193...3837)
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VVKTAEVTATIASAESLDKAVFIAVHDMAELFKKHTDLSTEGIATLFSTTGNAÇISQV
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complement(6324. .7776)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Best Blastp hit - gill0172637 dbj[BAB03744.1]
(AP001507) acetamidase [Bacillus halodurans], score 202,
E-value 3.008-51"
                                                                                                                                                                                                    /note-"pfam match to entry Transaldolase, Transaldolase, score 311.1, E-value 3.40E-92" complement(3851. .3855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /acte-"best Blastp hit " gill38145251gb;AAK41557.1.
(AE006746) Antibiotic ABC transporter, ATP binding
Protein (Sulfolobus solfataricus)', score 102, E-value
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5586, .6287
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5586. .6287
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3984. .3988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3997. .4896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="TTE1920"
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                                                                                                                                                                           'gene="MipB"
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                                                                                                                                                                                                                                                                                                                                                                                                                  4581 AGCCGTAGAAGTTGCTGGAAAAGTGCTTTTTAGAAGTGGAAGTCATAAAGGGATTGAATCT 4640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            946 TICCIGGCCACGAAIGGAGAAIGCCGAAAATATTAIGAGIAIIGGCAGIGCACGICCGCT 1005
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                                                                                                                                                                                                                                                     646 TGAAAAGGTCTACTGGAGCAAAGGCCATACGCTTCCCTAIAAACCCCATATTGGCACCTT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAAAGGTAATATTAATGAAAAACTAGCTCTTCCTGTAAAGCCAATGATAGGAGTAAT
                                                                                                                                                                                                                                                                                                                                                                           706 GAGCGTATCGCCAGAAATTGACTCAATCAATTCACTGACGCCAGACAATCACGCGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTTTGCTTGCTCTAGGGGACTTACACGCTTTAATGGGAGATGGAGAAGTAGGCGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATGGATGTGCCGGATATAGGACCAGGGAGTATTACCTATCTGCCGGTACGTGCGCCTGG
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                                                                                                                                                                                       Gaps
/gene-"PotE3"
/note-"Best Blastp hit - q1167594631emb|CAB69791.11
(AJ237785) putative amino ació transporter (Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS LMFLCHR36 Accession AL499624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /ranslation="MRQLLSLSSLTNSALLELVSGIVWRISLIFFKISSFFNSSIELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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   Genbank release 109; EMBL release 56.0; SwissProt release 38.0; plR-protein release 62.0; and Owiz release 31.4.

E-mail address for comments and questions: Kyutakkanite.go.jp ORF organization, sequence alignment and more information are available at W.W. w. site of Biotechnology Center.

URL: http://www.bio.nite.go.jp/dogan/genome_list-e.htmi/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="PIR:S74019 percent identity: 84.058 in 69aa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /producT-"368aa long hypothetical protein"
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                                                                                                                                                                                                                                           /organism-"Sulfolobus tokodaii"
/strain-"7"
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/qene="STS003"
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                                                                                                                                                                                                                                                                                                                                                                                                                complement(526. .1632)
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/gene="STS002"
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/gene="STS002"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene-"ST0001"
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LMFLCHR36_28 2800001 2910000

LMFLCHR36_29 290001 3010050

LMFLCHR36_30 3100001 3110000

LMFLCHR36_32 3200001 3100000

LMFLCHR36_33 3300001 3100000

LMFLCHR36_34 3400001 3510000

LMFLCHR36_35 3500001 3520000

LMFLCHR36_35 3500001 3520852

Continuation (2 of 36) of LMFLCHR36 from base 100001 (AL499624 Leishmania majo: chromose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100063 CGACCATGTATTTCCCCGTGGCCGTGCCAGGGGCCAACTTCACCGTGGGCGATCCGCATG 100004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100123 GCTCCATTCCGCCCAACCACACACACGGGGGAACATCGACAACTGGCGCATCGGCAAGGGGG 100064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100003 ceredeadadacecedaderardeaceaedacearedasraceceserakeeaacaan 99944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP000981 263050 bp DNA linear BCT 1:-CGT-2561 Sulfolobus tokodail genomic DNA, complete sequence, section:1/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                678 TTCCCTATAAACCCCATATIGGCACCTTGAGCGTATGGC---CAGAAATTGACTCAAICA 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Crenarchaecta: Thermoprotei; Sulfolobales: Sulfolobaneae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        735 ATTCACTGACGCCAGACAATCACGCGGGGAATATGGATGTGCCGGATATAGGACCAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            795 GTATTACCTATCTGCCGGTACGTGCGCCTGGAGGCCGCCTGTTIATTGGTGATGCCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       855 CTTGTCASGGTGAIGGTGAGATTTGCGGGACGGCAGTAGAGTTTGCCTCAAICACCACCA
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21456156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99943 TCCAGCTGGTCCTGCACAAGAAGGCGGACCTGCCTGGAACGCCGCTTGG 99836
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                                                                                                                                                                                                                                                                                                                         Length 110000;
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Kawarabayasi,Y., Tanaka,T., Hino,Y. and Kikuchi,H.
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                   135;
                                                                                                                                                                                                                                                                                                                  Score 56; DB 2; 1
Pred. No. 7.5e-05;
0; Mismatches 135
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Sulfolobus tokodaii
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AP000981.1 GI:15620945
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52.1%;
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172669 GATATTAAGCACTTAACTATAGGCACTAAATTATACCTTCCAGTATTTGTAAAGGGAGCA 172610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172729 GCATTACCATATAGAGGAAAATTGAGTACCATACCTCCTAGAGAAAACGGAGGAAATATG 172670
                  QVISGTMIPKSPLISTIIDSFGGKTAVSSPTGELSTEVARATAERV VATLCNTIPIQL
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9382. 9549
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                                                                                                                                                                                                                                                                                                                                                                                                              /Lranslation-"MKACTPSLLRENFIELIVMLTPISLRSSRRDLTLSPSROREQSL
CILNIYELFYI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCT 05-JUL-2002
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Piantes-Microcrganismes, UMR215-CNRS-IRRA, BP27, F-31326 Castanet,
Farance, Laboratoire de Genetique et Developpement UMR6061-CNRS,
Faculte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes,
France, GAIC GMbH, Fritz-Arnold-str. 23, D-78467 Konstanz, Germany,
            :DCKKILDDVRNAQPFRRLELVLKYLDPYTFNNFDFNEVKAIAERFVHYLCNTIP1QL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CapelalD. Barloy-Hubler, F., Gouzy, J., Bothe, G., Ampe, F., Batut, J., Boistard, P., Backer, A., Boutry, M., Cadieu, E., Dreano, S., Gloux, S., Godie, T., Goffeau, A., Kahn, D., Kiss, E., Lelaure, V., Masuy, D., Pohl, T., PortecialD., Puchlor, A., Purnelle, B., Ramsperger, U., Analysis of the Chicosome sequence of the legume symbiont Sinorhizobum melilot, strain 1021.

Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71) STATCSCCAGAAATTGACICAATCAATTCACTGACGCCAGACAATCACGGCGGGAATAIG 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sinorhizobium meliloti.
Sinorhizobium meliloti
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae: Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          770 GATGTGCCGGATATAGGACCAGGGAGTATTACCTATCTGCCGGTACG16CGCTGGAGGC
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                                                                                                                                                                                                                                               /note="OWL:AF072619 percent identity: 27.500 in 40aa.
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                                                                                                                                                                                                                                                                                                                                    hypothetical cytochrome b"
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AL591789.1 GI:15074950
                                                                                                                                                                                                                                                                               /codon_start-1
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PTKALAGDOTER:VRYYIEAGESVSKOVKGKTKIVEVYYGDVIKYIGDYSNYIOSVKR
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GIKPQIVIMSATLSDPEVVKPFFDVEIIGGKSERPANDTYIVLGKRDELMAISKALNV
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NLVGKLGGKVNYJGTAPVAVHHSGIDKYVROOVENDMRSGKLKVVVTVKTTLGGIDVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Swiss_Prot:040469 percent identity: 32.836 in 67am.mot.f-ATP/GTP-binding site motif A (P-100p)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene-"STS006"
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FEATURES

CDS

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(DECARBOXYLATING) PROTEIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFGAWNKGRLNSYLIEITEKVLKAADPLJGKPIVDMILLDKAGGKGTGKWSVIEAONMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                small molecules;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="cell processes; transport of amino acids, amines, peptides.
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GITEILAGTQYHLVVTPYSSAKDPLGPIRYILDTGAADGVIISRTE;NDFRVTL,TER
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Universitaet Bielefeld, Biologie IV (Genelik) Universitaetstr 25, 23.865 Rielefeld, Germany. Unite de Biechinle physiologique. Universite Catholique de Louvain, Place Croix du Sud 2, Btc 20, B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Paculte des Schences Agronomiques de Gembloux, Avenue Marechal Juin 6, B-5030 Gembloux, Belgium. E-mallicaromm.Gouzy@toulouse.inna.fr http://sequence.toulouse.inra.fr/mellloti.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function"cell processes; transport of small molecules"
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Gene name confidence: hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="PUTATIVE PERIPLASMIC BINJING ABC TRANSPORTER SIGNAL PEPTIDE PROTEIN"
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Gene name confidence : hypothetical
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predicted by Homology
predicted by FrameD"
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dene CDS CDS

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Nomura, N. aria Sako, Y. are at Kyoto University, Sakyo-ku, Kyoto 566-8502, Japan.
Nomura, N. aria Sako, Y. are at Kyoto University, Sakyo-ku, Kyoto 566-8502, Japan
The other authors are at the National Institute of Technology and Evaluation. 2-49-10 Nishihara. Shibuya, Tokyo 151-0066, Japan.
Ail the sequence with length 100 codons or more between ATG or GTG and stop codon are defined as CDS.
Accology analysis is performed by Smith Waterman algorithm against GenBank and Genept release 109; EMBL release 56.0; Swissprot release 36.0; PIR-Protein release 57.0; and OWL release 31.0.
F-mail address for comments and questions: genomcARD#inte.go.jp Restriction map, ORF organization, sequence alignment and more information are available at W.WW. site of Biotechnology Center, URL: http://www.milolinte.go.jp/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDDRDARNLAKKLGLQVMGTLGVIALAKYKGLTSKAKPIIDKLIESGFWISRRTEEFF
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Tcl:+81-3-3481-8951, Fax:+81-3-3481-8424)
Kawarabayasi, Y. is officially affiliated with the National
Institute of Bioscience and Human-Technology, Tsukuba, Ibaraki
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104aa."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22652 GTGGAGGGCGCCTGTTCTCCAICGGCGACACGCATGCGGCGAGGGGGGGGTGGCGAAGTC 22603
                                                                                                                                                                                                                                                                                   /protein_id="CAC46513.1"
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Submitted (14-DEC-1998) Yutaka Kawarabayası, National Estitutte of
Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10.
Shibuya-Ku, Tokyo 151-0066, Japan (E-mail: Kyutaka@kazusa.or.jp.
                                                                                                                                                                                                                                                                                                                                                                                                     AALAFHFKCLMLHRAPDGAPSSIAVVPLGGSDINSSKGLAIVGPDRIAAFPELLAGE
TIGARERIGAASWLETPLREMIGOTVPLH-VAVRAFAURIERAIRDASTPEREUGU
AAALGRISAARPPPDIAACHLOVGRSIVDDA RTILVRLIGTSBRILREH
GYGAKTLGRILRLORFLAAGRSRPGDTLANLAVDAGYADQAHLAREARGITSFTPREI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                878 TGGGGGACCGCAGTAGAGTTTGCCTCAATCACCACCATCAAAGTCGATTTGATCAAGAAC 537
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DNA Res. 6 (2), 83-101 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawarabayasi,Y., Hino,Y., Horikawa,H., Yamazaki,S., Haikawa.Y
                                                                                                                                                                                                     /evidence=not_experimental
/transl_table=11
/product="PUTATIVE TRANSCRIPTION REGULATOR PROFEIN"
     function="miscellaneous; not classified regulator"
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                          /note="Product confidence : putative
Gene name confidence : hypothetical
predicted by Codon_usage
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AP000059 BA000002
AP000059.1 GI:5103911
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0; Mismatches
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                                                                                                                 predicted by Homology predicted by FrameD"
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7796, .8239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SMc34265"
                                                                                                                                                                                /codon_start-1
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Tanaka,T., Hino,Y., Kar
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/product-"569aa long hypothetical protein"
/protein_id-"BAA79237.1"
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53.0%; Pred. No. 0.1;
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/codon_start-1
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AL132779.2 GI:6594223
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/LINIAWYFLAGRACAISFAYWYILGLSFTPCFRAFFIAWIGGG
LISLSFINSWYSFFECMSFLAMGSSASFSLFRSSRYALSYGGGSTASSYVYSTMY
WSICSRVWGGALSSWCCPFFLRFSSRSRMSPARFISSLLILPSFHWSDIGNELOY
WSICSRVWGGALSSWCCPFFLRFSRSRMSPARFRISSLLILPSFHWSDIGNELOY
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DXTIYIIINLCLLLUHLFPGIHTCPSKSQIEPPPEELLYRIDYLNMYLTLKRHNLSSG
         *KDEADADEAALADHESEKYKNVILLTWNKNDYTENCEKAYGVILYTPSDERVEVN"
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                                                                                                                                                                'hote-"similar to PIR:H69385 percent identity:39.175
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/protein_id="BAA79236.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="124aa long hypothetical protein"
/protein_id="BAA79234.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start~1
/transi_table=1.
/product~75aa long hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SFYILSNNELEELMKYMGCK"
complement(3752, .3979)
/gene="APES010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="APE0281"
comploment(4516..4842)
/gene="APE0281"
                                             Jomplement(3301. .3669)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3752, .3979)
/gene="APES010"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,5465)
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                                                                                                     comp.ement(3301. .3669)
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/qene-"APE0282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4628. .4402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  table-11
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4831. .6840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"APE0282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4831. .6840
/gene="APE0283"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="APE3280"
                                                                                                                                  /gene-"APE0279"
                                                                                                                                                                                                                                 /codon_start |
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                                                                        /gene+"APE0279
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/transl_table
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/transl_table
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                                                                                                     CDS
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/transl_table=11

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151824 ACGGAGGAAACCTCGATGTGAGGCACTTCTCCCCAGGCTCCAAAATCTACTTCCCCGTGT 161765
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                                                                        LTREOIDOY IVOTTI DEAYEOLOAEYORAY RELGKREKEAEDPHIKKLIONIKEYHEL
FRKDNEMRPPWMLTAILLNEALKHGVKDRDX IYQY II.KASWEY AKEIAOALPAKKYOG
RYTRAYADOMRNPFISI IEIEAMI REANRDDPKWKKYTQMFDI,YWNKIPDDIYNRADS
                                                                                                                                                                                               OHHEVTKY:JOLLEEAIREAERESGVEPFWHKTPEFILGIGFGEPAFAGFPILAYPDR
YDLAQKVLIKTIVLGFEFEGGGYHROLYRAENLIDSPITTHWWYPETAWFENLE
KGRHYSPLYOLJGXLPWPELKOGRYRYLAOIEOGKSISEIPEERKKFRFUTELKN
EIWRNDDRFYPIVEELYATGWIKDAAKTLGVLDDFAKIYSGEKSPRQAGIERDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSGTCPGRRVSALPPARDPLPVLCRGFPRGSCARRALPPIPFLP HEGPLPGVAGILLLHDAASRPYYRCRPESCSNTDQTSVX1FSTSDHPCLLLLSSPRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLN 15-DEC-1999
                                                                                                                                                                                                                                                                                                                                                         QVLHVIKNLRDKGNYVDPYHVTFILINIJEQHIQDPLLREAYKRILEHYQRTHGEJPR
DLRYLERVVFEERELEEKLKGLFRENRKLSEGDIRRTAMI,YRTLMLLTPHPSLEDIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                      FYSRLAERLKVKVGEESFLPVHGPVAEDVASSFAAIRRAKPEERERVVRREISGFEPL.
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/trans:ation="MGDHRGDGRMSRELIGLGAGILIRILLKNLKKKGQHIEERAPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      756 ACGCCGCGAATATGGATGTGCCGCATATAGGACCAGGGAGTATTACCTATCTGCCGGTAC 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and Department of Biological Sciences, University of Exeter, Perry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hunt, C., Aves. S., McDougall, R.C., Rajandream, M.A. and Barrell, B.G. Direct Submission
Submitted (02-NOV-1999) European Schizosaccharomyces genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCGCCTGGAGGCCGCCTGTTTATTGGTGATGCCCATGCTTGTCAGGGTGATGGTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTGCGGGACCGCAGTAGAGTTTGCCTCAATCACCACCATCAAAGTCGATTTGATCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 157000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"102aa long hypothetical protein"
/protein_id-"BAA79238.1"
/db_xref="G1:5:03922"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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COMMENT

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/traislation-"NEWSFULSSNAALVQHLVESKELTNORAIKAMNATSRSFYCELS
PKDSPOSIOYGVTISAPHMIATALOLEDVLQPGCSALDIOSSGSGTVAAMARNAP
NGTVKGIEHPOLVETSKKNLLKDINHDEVJAEWYKERLOTNOGENGTSEDEKFD
NITVKGIEHPOLVETSKRNLLKDINHDEVJAEWYKERLOTNOGENGTSEDEKFD
AIHVOASASELQQKLUSOLKSPGKILLFPIGTYSQNIYLIEKNEGGKISKRTLFPVRYV
                                                                                                                                                                                                            RHVOLIAIGGCIGTGIFVGSGSÄLSESGPÄSLFLSYVIMSFYWTVMNALGEMCTYLP
LSGASPITYIERYVDASLAFAAGWNYWYAYVFLVASEVTAASIVIEYWTYAVFTAGWI
AILLFLVAVLNSFFVKWFGETEFWFAIIKVIAIVGLIILGVVIFFGGTPKHDRLGFRY
WKHGLAFREYIVKGASGRFVGFWSAVIKSGFAFILAPELVIFSAGETFAPRRNIPKAT
                                                                                                                                                                                                                                                                                                                                                                                                        ACLAFLNASASAAVVENWECNLSTISSFLAWICVLVAYLOFKRAMILNNLWETRRYKT
PFQPYAIYLTLELLALITLINGFTVEVGHTFTAGNFIAAYITLDIFLVLYVAHKLWSR
NWSFGKRIEEISVTIGVAEARALEOMYPAPVPRNIIEKIWFWIA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /noie-"SPAC869.09, len:116, SIMILARITY:Schizosaccharomyces pombe, YAAB_SCHPO, hypothetical 15.4 kd protein c2297.11c in chromosome i., (140 aa), fasta scores: opt: 192, E():2.5e-66, (39.6% identity in 139 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MPDPAHIIAGHKAALSNPHVSEEAKFRARKYLKEHGSESHYTG
TTRGGRADADDAGELREGFGTKNQFEDNESGAKNIGNVRGGYKAAMHNPKVSGKGRR
HAKE:...FEVDDESK"
                                                                                                                                                                                                                                                                                                                                                  SRF IYRLIFFY IFGSLTIGVITSSKOPRLLNA I SSGASGAAASPFVIGIQNAEI PVLN
HIINAVILITSACSSGNSF IFAGSRSIYSLAKEHQAPKIFKYCNRWGVPVISVAVTVLF
                                                                                                                                                                                        /translation="MDEKKALQYEESKRABEITDIELVSVGGIDVEKKYGETKRALKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Match to PF00324 aa_permeases, Amino acid permease Score 718.22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SPAC869.08"
/notc-"SPAC869.08, len:230, SIMILARITY:Triticum aestivum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PINT_WHEAT, protein-l-isoaspartate o-methyltransferase, (230 aa), fasta scores: opt: 602, E():2.2e-32, (48.5% identity in 250 aa)" (codon_start_l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein-1,-isoaspartate(D-aspartate) O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /hote-"SPAC869.07c, len:436, SIMILARITY:Mortierella vinacea., Q02402, alpha-galactosidase, (417 aa), fasta scores: opt: 1443, E():0, (52.3% identity in 407 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative protein-1-isoaspartate o-methyitransferase"
/protein_id="CaB60018.."
/db_xref="G1:6224599"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"putative alpha-galactosidase"
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                                                                                          /product-"amino-acid permease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Match to PF01135 PCMT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7524, 7874)
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/noie<"SPAC869.09, len:116,
                                                                                                                     /protein_id-"CAB60020.1"
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/note="Mat-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene+"SPAC869.09"
complemen*/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(8756. .9448)
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complement(8756. .9448)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6788. .7138)
/note-"TF1 LTR"
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10265. .11575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3816. .5228
/gene="SPAC859.10c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=SPAC869.07c
                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=SPAC869.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label-SPAC869.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGSSCG4SGTJ9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   done
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.12
                                                                                                                                                URLA, http://www.sanger.ac.uk/Projects/S_pombo/)
During 1995 to 1996 about 668 of S. pombe chromosome 1 was
During 1995 to 1996 about 668 of S. pombe chromosome 1 was
sequenced by the Sanger Centre. The Sequencing of the S. pombe
genome is now being costinued with funding from the European
Commission. Fourteen European sequencing laboratorics, including
the Sanger Centre, are participathing in the project.
Protein coding regions (DS) have been predicted with the help of
computer analysis using the Genefinder program in Pombase (an ACEDE
database) with additional predictions for the branch-acceptor sites
supplied by the program SpSaplice. To the branch-acceptor sites
supplied by the program SpSaplice. To the branch-acceptor sites
any individual CDS we may have underestimated or overestimated the
number of introns/exons or we may not have chosen the correct
splice donor/acceptor sites.
Complementary strand.
In more significant matches with motifs in the PROSITE database
The length in codons is given for each (CDS.,
The length in sequence MAY NOT be the unlike insert of the
sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SPAC869.11, len:536, SIMILARITY:Schizosaccharomyces
pombe, ISP5_SCHPO, sexual differentiation process putative
amino-acid permease isp5., (543 aa), fasta scores: opt:
1812, E():0, (53.9% identity in 492 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MEPEYVSFSDKDTKSILNESKSSLKDVKPSLEEKSYITPGLVDD
VEPKGKNFVVRFFDDFKPAKATGEDGTALKRSLKSRHMQMISIGGAIGTGLYVGSGSS
LADGGPASVIINYSLIGIMMFFIVYALGEMAVAYPVAGGFNTYATRFIDFAWGFAVSW
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STSVSPFVLAIKEANIKGLPSVFNAV.11SVVSVTNSSTYTAGKTLHGMANLKOAFSF
FKYTDRIGRPLLAM:VVLLFGFFAYINFADKNGNDVSDTVFNWLLALSGESNFFTMGS
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STVKVVATFGFIILAIIINCGGVPIDHRGYIGGSIIKHKPFRHGFKGFCSVFTTAAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICLCHIIFRLAFKKQGHSLKELGFVSPMGIWGSCIGLFFNILCLMAQFYVSLFPIGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nidulans, PUTX_EMENT, proline-specific permease, (550 ag),
fasta scores: opt: 1968, E():6, (53.3% identity in 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Details of yeast sequencing at the Sanyer Centre are available on
the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequenced clone. It may be shorter because we only sequence overlapping sections once, or lorger, because we arrange for small overlap between neighbouring submissions.

Location/Qualifiers
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                              Dec 16, 1999 this sequence version replaced q1:6224591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 114;
/note*"Overlap wit; c922 S. pombe chromosome :"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism "Schizesaccharomyces pombe"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product~"amino-acid permease"
/protein_id-"CAB60021.1"
/db_xref~"GI:6224602"
EX4 4CG, United Kingdom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1...1610)
/gene="SPAC869.11"
complement(1...1610)
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3705, 5342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome-"I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start-
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/translation-"msvydeyldnikgwrirkaleivrrkeeklevikralgekdpl
vkkgtlyiikklamkkelsyneirelmpslikleddkdesvvlotvetinaiinfmdl
pkkgtlyiikklytrenepineyaaegvatloriinfrifsmirgilogres
rkkysalrykelvytrknememeerenlaldvindedpvrstalkiibvaldrres
lsreslekasamlosssigketkekideilogreekkvktevsvdysysvetikemeer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MKVIKENNVKVKLVRTKRGAILHWIELKPGHFFLEONPLKPSKY
GEATRIKONFPEFYFFWEIKDNKYTGRILAGAFLEKEEIDEFLTLLAKTEDFKKLEH
VLEEIEEDEDEEEE
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DKNETVORNTLFVIRKLIKDGKLDSEQDTELLDIIRLSKSSNBKIALANSLKCHETLD
DNVOLSNGSYDKVINTLSGTRRETIRRSTAREELGILGAKITSFTKRIVEFLVSLI
KEGRDREVGAALGALTEIAARSDNVEVIEDITREIREFIKTEQDAELKKKAISSLEI
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GILKKVVEMLSSKEYIRRADALMVIARIIKFLDPNMARYVVKNLAGLVKDRNPWIRNT
AIKAIAEAYVLYPEVRMDVIPLLDALLRSNNKEDVELALNIIKEILSYSHDEELFRAT
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EEFILAYNPWVRSTSAKVLADLALEYSSIMEREISKALFLIESNDEKLVIAGIELADA
LLSRIKNIGFLREVMKRLIRKDRLPREALDFIKKYESYIEELEPEIKROISKLVNSL
                                                                                                                                                                                                                                                                                                                                                     DKDKFIYGVGASVPPHIQKPEERKKAPEMDQIFIDIGAESKEEAEEMGWRIGTVITKD
GRLERLGKHREVSIAPDDRIAYTMLEVARQLEDTKADVYFVATVQEEVGLRGARTSA
FAIEPDYGFAIDVTIAADVPGTPEHKQVTHLCKGTAIKIMDRSVICHPTIVRMLEELA
KKYEIPYQLEILLGGGTDAGAIHLTKAGVPTGALSVPARYIHSNAEVVDEROVDATVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation-"MYPMNPKQLKKLMKQLDMKQLDGVKEVIIKLENKEIVIKEPVVT
VIRAMGEKMYQIAGGTEEERVVLKISEEDIKLVMEQAGVDYETAKKALEEAGGDLAEA
                                                                                                                                                                                                                                                                                                             /translation-"WVNYELLKKVVEAPGVSGYEFLGIRDVVIEIKDYVDEVKVDKL
GNVIAHRKGEGPKVWIAAHMDOIGLMYTNIEKNGFLRVAPIGGVDPKTLIAQRFKVWI
                                                                                                                                                                                                                               /product-"aminopeptidase from family M42"
/protein_id="CaB49557.1"
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/anticodon=(pos:601906. .601908.aa:Leu)
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                                                   /organism-"Pyrococcus abyssi"
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/note="PAB1939"
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/product="hypothetical
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                                                                                              /db_xref-"taxon:29292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"tRNA-Leu"
Cocation/Qualifiers
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/transl_table=11
                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1188. .1535
/note-"PAB0438"
                                                                                                                                                         /note: "PAB0437"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LMVKALENIHELKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PAB0439"
                                                                              /strain-"Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start-1
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                             source
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  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation ""MLQYSKKKVSLNFFPVRLLSYKMTRISDAIFKDHRKLGSDYQNI
KRANDYDTATRWONDFWDRALBAHSVSEBIVVYFRFRYTGESCKEMAEKGRHEHGLYK
EMLYKFOSMKANOSRTPALDELMESLGKHIDEEEGHD!PFLEKHLSEFESLHKASSF
ERTKKFVPTHSHPSAPNKPPFETVAGI.FAAPIDKI.ROMMEKWP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Schizosaccharomyces pombe, SULH_SCHPO, probable
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                                                     CDIDESTILMNAKAIKEEGLLDLGYEYIVMDDCWSKHERNATIGKLEANPDKEPNGIG
SMAKKLBDMGFKFGMYSSAGKYTCAGFPGSLNHFQIDADIFADWGVDYLKYDNDFNBG
KSGVPLISYERYKRMSDALNKFGRPIFYSLCQMGEDFVWNWGNTLANSWRISGDIFDT
                                                                                                                              FSKKDVRCPCETIECFALOGDHCSVRNIISKASFISSRAGMNSGWNDILSIEVGNGGM
SKEEYKTHTFWALIKSPLLIGNDVSSRSPMNKLIVENKELISINQDIGINFAALIWK
KKODEZIELFSGRIANDWVVAVINAASEPIKMGIHISDIEVDALGNAFHDWIATDI
WNNNVKLVSDRIRANVASHGVQWWRPQQYKVKNINDKFFSFNKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sulfate permease spbc3h7.32., (877 aa), fasta scores: opt:
3127, E():0, (62.8% identity in 827 aa)*
                          /translation "MISISFLNGFT,VFLFH,FFSDVFGSYNGLGLKPCMGWNSWNKYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (06-UUL-1999) Genoscope - Centre National de Sequencago
BP 191 91006 EFRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
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21
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X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               789 CAGGGAGTATTACCTATCTGCCGGTACGTGCGCCTGGASGCCGCCCGTTAATTGSTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      729 CAATCAATTCACTGACGCCAGACAATCACGGCGGGAAIATGGATGTGCCGGATATAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Thermococci; Thermococcales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30/120 pp DNA linear Pyrococcus abyssi complete genome: segment 3/6. AJ34828 AIndéas4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
/protein_id="CaB60016.1"
/db_xref-*GI:6224597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22092 TTCATTTTCTCAAGGTGATGCCGAAATII 22063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.63;
0; Mismatches
                                                                                                                                                                                                                                                          /gene~"SPAC869.06c"
13058. .13669
/gene~"SPAC869.06c"
/note~"SPAC869.06c, len:203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      len:840,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               849 CCCAIGCTIGTCAGGGTGATGGTGAGATTT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sednence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SPAC869.05c"
/note="SPAC869.05c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermococcaceae: Pyrococcus.
1 (bases i to 307120)
Heilig,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3127, E():0, (62.8%
/codon_start=1
/label=SPAC869.05c
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/label=SPAC869.06c
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AJ248285.1 GI:5458067
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Similarity 55.3%;
83; Conservative (
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Pyrococcus abyssi
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CNSPAX03
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282090 ACCCCAGGAAAACACGGCGGAAACATGGACAAAACCTAATCAGAAAGGGAACCACCATT 282149
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IXTIREKYGKSPVDVLEDVGLLNEKLIAAHGTUSDBOIRKISSAGATHAICPASNMK
LGSGVFPMKAALENVOLLOKLILAAHGTUSABOBOIRKISSAGATHAICPASNMK
LITOKSTOFPMKAALENVOVALGTDSASNNTLDILEBRILASLLOKYTHRDESIVKSED
IFRMATLNGAKALGIKAGVIAEGYLADIAVIDLRRAHJI,PVNSPLASIIFSAHGGUVI
11.10GGELWMLDSELLTVDEEKVIDKFLEVSVA*

7.10516

/nole**PAB0444*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /traislation-"MIPFFKEVLMGIPPLVIYVVLFYHYHISRNSSYLMYFSLAFISL
GVGIMVEDAYLAGLAFFSSFFWIGVIQFLRRIGGFKGLNLKYLLYVARTSLASYMFFL
DRSEVITU-YSLMATLLARIAFKKYKTSVFLYLLVLVVSYGYYSDLAKYLFVIIA
TILGYFLIVETKOLKKTILSPFGFELKLKPGVIFAETIPEDILKVALVFSRKPGK
GERRFWYTKLKSSPWTIEPTNLPKLISLAPDYLKKRGVVTICLDYLILENGFESVI
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GSKLALIEMAHSGTSTFVDMYFHMEEIAKATEEVGLRAYLGYGMVDLDDEEKRKIEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVSEYIRISKEEMRKOIGRDWIEHGEVVVTPPLNLAKNGVKYVIHTVGPYGGGKWDED
KRKKLELAILGALKKADELGVRSIAFPAISAGIYGCPLEEVVKIFKLVVNEFLKSAKN
VTDVYLVLYSERDYEVALKVLERDEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mrkmfrvvhgdltrfkaealvnaankylehGGGVaYalakaasG
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ALI62753 ALI57959
ALI62753.2 GI:7379120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill, J., Achman, M., James, K.D., Bentley, S.D., Churcher, C., Klee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Davies, R.M., Davies, P.W., Peltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K., Cuail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G. Compiete DNA sequence of a serogroup A strain of Nelsseria meningitidis 22491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCTGCCGGTACGTGCGCCTGGGGCCGCCTGTTTATTGGTGATGCCCATGCTTGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 307120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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/db_xref="GI:5458080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"hypothetical protein"
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/db_xref="GI:5458079"
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0; Mismatches
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Neisseria meningitidis 22491
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/transl_table-11
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/transl_table+11
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53.8%;
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Best Local Similarity 53.8
Matches 85; Conservative
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/db.xref="Griss" (3458076")
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SGFEGLGEGKKVEDOLVETARKYOHNIGPNYTTARKLOFFGTPVLPGFLA
LISOSGAGIALMGWTILEKIGLSAVVSVGNKADIDDADLLEFKDDDTFRILITYWE
GVKGRRFNEYAKKPYSKKRPTIVIRAGRSERGAKAAASHTGS.AGSDITYSAAFKQSG
VLRALTIGEAFDWARALSNLPFPQGDNVVITYNGGGIGVMATDAAEEEGIKLYDD.EO
LKITAHMPPFGSYNNPVDLTGMADAKSYEGAIRDALNHPEMISITVLYCQTAVLDPR
DLAEIIIREYNESGRKKPLVVAIVGGIEAKRAIDTLNBNGIPAYPEPERAVKALSALY
RWSKWKAKHK"
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| Abxret="4115458074"
| Aranslation - WARRPEDTO | WARRPEDTO | ABAIRDOGENTHESTREET | ABAIRDOGENTREET | ABAIRDOGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="LSU ribosomal protein L37E (rpl37E)"
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RLRRYRWSKKWKKKNNH"
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TAKLTPNVSDI REI GLAAFKAGAJGVSA I NTVKA I AI DI YAKRPILLSNKFGGY SGPGV
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IAEGISRYLKEEGYSSVKEIIGLAUKV"
LITIKKLDDKSIRPYILGFYALVADNFLNVDIELIRVLIGKLNETYKDLTQDFKKTA
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/product="chlorohydrolase, putative"
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/note="PAB1937"
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/genc-"neac"
/note="PAB0443"
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/product="snRNP,
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/genc="rpl375"
/note="PAB7166"
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5646, con
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/codon_start-1
                                                                                                 'note-"PAB1938"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5407. .5634
/gene="snrnp"
/note="PAB8160"
                                                                                                                                                                                                                                                                                                                                                                                 /codor_start=1
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Translation-minivory wildlestry wilds the second and se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
/product="very hypothetical protein NMA0372"
/protein_id="CAB83673.1"
/brotein_id="CAB83673.1"
/db_xret="G1:7378MB1:09JWH3"
/db_xref="SPIRMB1:09JWH3"
/translation="MFGRLSPLGSDGFFLAVYEYPVGFICLQGKTAYFRSGGKRFHRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //note="NMA0373, thif, probable Thif protein, len: 256 aa; similar to e.g. THIF_BCOLI P30138 THIF protein (251 aa), stasta scores; E(): 0, 43.14 identity in 246 aa overlap, and MOBB_BCOLI P1228 molybdopterin biosynthesis MOBB protein. (249 aa), fasta scores; E(): 0, 43.9% identity in 244 aa overlap (note that N.m. does not have orthologs of any other molybdopterin biosynthesis proteins). Contains pfam match to entry PF00899 ThiF_family, ThiF family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"SLYX protein homolog"
/protein_id-"CAB83672.1"
/db_xref="G7:7379124"
/db_xref="SPTREMBL:09JWH4"
/db_xref="SPTREMBL:09JWH4"
/db_xref="NDAVQEFEBRITELEIQSALQEDVIAGLNAMVAELRQTLDLQQA
                                                                                                                                                                                       /note="NMA0370, probable integral membrane protein, len:
62 as, similar to hypothotivel proteins e.g. 7325_HABIN
P44640 hypothotical protein H10325 (450 as), fasta scores;
E(): 0, 49.8% identity in 464 as overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aa.
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/gene="NMA0372"
/note="NMA0372, unknown, questionable CDS, len: 50
//codon_start=1
                                                                                                                                                                                                                                                                                                                                                                               /trans__table=11
/product="putative integral membranc protein"
/protein_id="CAR83671.1"
/db_xret="G1:7379123"
/db_xref="SPTREMBL:09JWH5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3562. .3571
/note="Core DNA uptake sequence: gccgtctgaa"
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/transl_table=11
/product="ThiF protein"
/protein_id="CAB83674.1"
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/gene="thit"
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/gene="NMA0372"
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/gene="thif"
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/transl_table=11
                                                                   /gene="NMA0370"
1578. .2966
                                                                                                                                           /gene="NMA0376"
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/gene="slyx"
2967. .3191
/gene="slyx"
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/db_xref="G1:7379121"
/db_xref="ST:7379121"
/db_xref="stranslation="MORONGSSPIVMLLVSVALWIASLSNVAFYLGNHGSWEGLTV
/translation="MORONGYSPIVMLLVSVALWIASLSNVAFYLGNHGSWEGLTV
LIGSTFASLDIRYCAYANYWLAA.VLLALRKKVVPHAAFWGLALVAFSVKAVYV
DEAGNTSDIVRYGAGFYLWYAAFAVASIGTFAGKNKERKAASAADGTKNOV"
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too e.g. HEMK_ECOLE 97186 HEMK protein (277 aa), raska
scores: E(): 9, 42.3% identity in 279 aa overlop. Contains
PS00092 N-6 Adenine-specific DNA methylases signature
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RQRADRLAQRRI NGBPVAY II.GAREFYGRRFTVNPSVI.TPRPETBHIJVBAVLARIIPEN
GRVWDLGTGSGAVAVTVALERPDAFVRASDISPPALETARKNAADLGARVEFAYGSFF
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DRLAEGGFLLLEHGRDQGAAVRGVLAENGFSGVETHRULAGLDRVTLSKYMKHLK"
831. .840
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/note="AIR repeat; hnmfs hit to HMM AIR (1 - 183), score:
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/gene="NMAA0368"
/fore=="NMAA0368"
/note="NMAA0368" probable integral membrane protein, ien:
153 aa; contains four probable transmembrane domains"
                                                                                                                                                                                                                                                                                                                                                                                       Centro are
                                                                                                                                                                                       Direct Submission
Submitted (30.MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Weilcome Trust Geneme Carpis,
Hinxton, Cambridge CB16 1SA E-mail: parkhill@sanger.ac.uk
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Details of N. meningitidis sequencing at the Sanger Cent.
available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
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/gene="hemk"
/note="Core DNA uptake sequence: geogretygaa"
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/note="Core DNA uptake sequence: gccgtctgaa"
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/strain="22491"
/db_xref-"taxon:122587"
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/db_xref="G1:7379122"
/db_xref="SPTREMBL:09JWH6"
Nature 404 (6777), 502-506 (2000)
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/product="HemK protein"
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1. 349061
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/transl_table=11
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220. .681
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                                                                                               2 (bases 1 to 349061)
Parkhill.J.
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1162. .1:71
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                /db_xref-"Sptremal.:09JWH2"
/translation="MTTTEHDNDDAFLLRYSRHILLDEIGIEGOOK.SAAHJIVVGCG
GLGAALPYLAASGIGTLIADSDTPEHNLORYAPERGOVGKLKTFALADHIRHIN
TYDVRTINKLDGCTJGLVOAADIVLDCDDAFTROAVRACVOAKTP!VSGAAVE
PROGOLAYYRDLPDSPCYACEPOGGSASGIGSLFOYPSPLVGTIGSTQAASTALLL
DAGEPSHGRLAVYRALEGGWQYFDLPRNPECPVCGAER"
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//Acte-"NMA0374, ppc. phosphoenoipyruvate carboxylase, ien: 917 aa: smlar to mary e.g. CAPP_RHOFA 032483
phosphoenoipyruvate carboxylase (RC 4.1.131) (936 aa), fasta scores: E(): 0, 43.3% identity in 928 aa overlap. Contains 2x Pram match to entry PF00311 PRPcase, Phosphoenolpyruvate carboxylase, PS00017 ATP/GTP-tinding site monif & (PLOOP), and PS00393 Phosphoenolpyruvate carboxylase, active site 2
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                                                                                                                                                                                                                             /note-"pfam match to entry P700899 Ihit family, Thir family, score 186.60, E-value 4.1e-52" complement(4418. .4427) /note="Core DNA uptake sequence: gccgtctgaa" /label=DUS
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                                                                                                                                       3787, .3796
/moter"Core BNA uptake sequence: gccqtctgaa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //product="phosphoenolpy:uvate carboxylase"
//protein_id="CABB3675.1"
//db_xref="G1:7379127"
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Pred. No. 2.9;
0; Mismatches
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Sequence 814 from Patent WO0065062.
AX041919
                                                                                                                                                                                             complement(3847. .4257)
'db_xref-"GI:7379126"
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447: 7224
/gene="ppc"
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Rest Local Similarity 53.0v
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Pyrococcus abyssi
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                                                                    sequences) New Sequences: seq 001, from 0.000.001 0.349.980, length: 349.980 seq 813, from 0.000.001 0.649.980, length: 349.980 seq 814, from 0.500.001 0.249.980, length: 349.980 seq 814, from 0.500.001 0.249.980, length: 349.980 seq 816, from 1.200.001 0.549.980, length: 349.980 seq 816, from 1.500.001 0.559.980, length: 265.118*
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tive 0; Mismatches
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		K. Oxvtoda 3-sport	Enteropactor close	Enteroberter close	DATOCOCCE abases	CP] death hid obs	Drosophile melanos	Drosophi'a melanog	FO W Dit, builder N	Neisseria meningit
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                                                                                                                                                        This DNA sequence encodes a R-specific amidohydrolase isolated from Xlebsiella cxytoca strain PRS1 which allows the microorganism to utilise 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel amidase, and the gene encoding the novel amidase, from Enterobacter cloacae. The novel amidase stereoselectively hydrolyses alpha-amino acid amides and alpha-hydroxy acid amides to give optically active alpha-amino acids and alpha-hydroxy acids. The invention also relates to variants of the novel amidase which retain activity, recombinant vectors and host cells containing the novel amidase gene taken activity and more amidase. Genetically manipulated microorganisms comprising the novel amidase gene have remarkably elevated catalytic capability as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compared to those produced by conventional methods. The present sequence represents DNA encoding the novel Enterobacter cloacae amidase.
                                                                                                                                                                                                                                                                                         Novel amidase gene encoding protein which stereoselectively hydrolyzes alpha-amino-acid amides and alpha-hydroxy-acid amides, with enhanced catalytic capability to yield optically active alpha-amino-acids and alpha-hydroxy-acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTAICTGCCGGTACGTGCGCCTGGAGGCGCGCGTGTTATTGGTGATGCCTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              893 TATGGCTACCGGTGGAAGTAGAAGCGCGTTGTTTTCTATTGGTGACACCCACGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.4%; Score 49.2; DB 21; Length 1444; 11.4%; Pred, No. 2.38-05; O; Mismatches 109; indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hyperthermophilic archaeon; hyperthermophilic protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             921 TCGATTIGATCAAGAACTGGCAGCTTTCCTGGCCACGAATGG 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1444 BP: 270 A; 422 C: 450 G: 302 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                         Example 1: Page 26-29: 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus abyssi genomic fragment #3.
                                                                                                                                    (MITR ) MITSUBISH! RAYON CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH41224 standard; DNA; 349980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.48;
                                          17-APR-2000; 2000WO-JP02492.
                                                                                       99JP-0109328
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Rest Local Similarity 51.49
Matches 114; Conservative
                                                                                                                                                                                                                         WPI; 2000-672731/65
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                                                                                                                                                                                                                                                 P-PSDB; AAB29631
                                                                                       16-AFR-1999;
                                                                                                                                                                                 Nakamura I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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26-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          741 TGACGCCAGACAATCACGGCGGGAATATGGAIGTGCCGGATATAGGACCAGGGAGTATA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      552
                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel amidase, and the gene encoding the novel amidase. From Enterobacter cloacae. The novel amidase stepulation of the novel amidase distributely hydrolyses alphalamino acid amidas and alpha-hydroxy acid amides to give optically active alpha-amino acids and alpha-hydroxy acids. The invention also relates to variants of the novel amidase which retain activity, recombinant vectors and host coils containing the novel amidase gene, and recombinant production of the novel amidase gene have remarkably elevated catalytic capability as compared to those produced by conventional methods. The prosect sequence represents the DNA coding sequence of the novel Enterobacter cloacae.
                                                                                                                                                                                                                                                                  Novel amidase gene encoding protein which sterepselectively hydrolyges alpha-amino-acid amides and alpha-hydroxy-acid amides, with enhanced catalytic capability to yield optically active alpha-amino-acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         801 CCTATCIGCCGGTACGTGCGCCTGGAGGCCGCCTGTTTATTGGTGATGCCCATGCTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         861 AGGGTGATGGTGAGATTTGCGGGACCGCAGTAGAGTTTGCCTCAATCACCATCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533 TATGGCTACCGGTGGAAGTAGAAGGCGCGTTGTTTCTATTGGTGACACCCACGCCGCUC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.4%; Score 49.2; DB 21; Length 945; Best Local Similarity 51.4%; Pred. No. 1.7e-65; Matches 114; Conservative 0; Mismatches 108; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amidase, stereoselective hydrolysis: alpha-amino acid amide; alpha-hydroxy acid amide; optically active product; recombinant production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              921 TCGATTIGATCAAGAACIGGCAGCTTTCCIGGCCACGAATGG 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 945 BP: 169 A: 283 C: 286 G: 205 T: 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacter cloacae stereoselective amidase DNA
                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 23-25; 32pp; Japanese
                                                                                                            (MITR ) MITSUBISHI RAYON CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC64149 standard; DNA; 1444 BP
                17-APR-2000; 2000WO-JP02492
                                                               99JP-0109328
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                                                                                                                                                                                                  2000-672731/65
                                                                                                                                                                                                                                                                                                                                      alpha-hydroxy-acids
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                                                               16-APR-1999;
                                                                                                                                                       Nakamura T,
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RESULT 3 AAC64149

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282450 FACTICCTGTICGTIGATGGASCTTACCTCGCIATAGGCGATTIGCATGCGTAATG 282509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyssi. The 5' end of this sequence overlaps with the 3' end of AAH41223 and the 3' end of this sequence overlaps with the 5' end of AAH41223 proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     743 ACGCCAGACAATCACGGCGGGAATAIGGATGTGCCGGATATAGGACCAGGGAGTATTACC 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       803 TATCTGCCGGTACGTGCGCCTGGAGGCCGCTGTTTATTGGTGATGCCCATGCTTGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: This patent is in the same patent family as WC200055052, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell death; head involution defective; hid gene; reaper gene; rpr; apoptosis; transgenic animal; antisense; ss.
                                                       '5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 2.9%: Score 41.2; DB 22; Length 349983;
Local Similarity 53.8%; Pred. No. 0.39;
Les 85; Conservative 0; Mismatches 73; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 349980 BP; 94090 A; 78692 C; 78319 G; 98879 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                   New nucleotide sequences isolated from Pyrococcus abyssi encode
                                                       end
                                                                                                                                                                                                                                                                                                  Lecompte 0;
                                                       'n
                           /*tag= b
/no.e= "This sequence overlaps with the
AAH41225"
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                                                                                                                                                                                                                                                                                                Thierry JC, Prieur D, Dietrich J, 1 Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                           (CNRS ) CNRS CENT NAT RECH SC1.
(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 347-443; 1657pp; French.
                300001..349980
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AAQ66950/c
1D AAQ66950 standard; cDNA; 3900
                                                                                                                                                                          99FR-0005034
                                                                                                                                                                                                           99FR-0005034
                                                                                                                                                                                                                                                                                                                                                                                                     proteins useful in industry
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AAH41223"
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                                                                                                                                                                                                                                                                                                                                                WPI; 2001-126236/14.
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                                                                                                                                                                                                                                                                                                Forterre P,
Querellou J,
                  misc_feature
                                                                                                      FR2792651-A1
                                                                                                                                                                          21-APR-1999;
                                                                                                                                                                                                          21-APR-1999;
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                                                                                                                                       27-OCT-2000
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1458 ACCACCGGACIGGCTGICGGTAIGGCAGACTGGAIIATTGCIGCTGCTGCTCGAGTGGCTAII 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 ACACCCGICCTGACCATCGAACCCGGIGACCGGATTATIGICGACACTCGAGAIGCTITT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 GAAGGTGCTATCAATTCGGAACAGGATATTCCGAGCCAGTTGCTAAAAAIGCCCTTTCTC 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 AACCCACAAAACGGACCGATCATGGTCAATGGCGGGGAGAAAGGTGATGTGCTCGCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           The reaper (rpr) and head involution defective (hid) genes, mapping to position 75C1,2 of D. melanogaster chromosome 3, exhibit expression patterns related to the pattern of cell death during Drosophila embryogenesis. Cell death genes, or antisense sequences, can be used to reduce or abolish apoptosis, e.g. in transgenic animals. An hid cDNA sequence is given in AAQ66950, and the deduced sequence of the encoded HID protein in AAR55791.
                                                                                                                                                                                                                                                                                                                                   Solated cell death genes from Drosophila - and novel assays for apoptotic cell deaths and apoptotic and necrotic cell deaths, based on selective staining by toluidine blue, acridine orange and Nile blue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dresophila melanogaster expressed polynucleotide SEQ ID NO 21221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orosophila, developmental biology, cell signalling, insecticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.7%; Score 39.2; DB 15; Length 3900; 49.1%; Pred. No. C.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3900 BP; 1288 A; 876 C; 736 G; 1000 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 TATATCGAATCCA;GTTGCCCCGCGGGGGTTGA 531
                                                                                                                                                                                                                                                       Abrams JM, Grether ME, Steller H, White K;
                                                                                                                                                                                                                      (MASI ) MASSACHUSETTS INST TECHNOLOGY.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure: Fig.6; 93pp; English.
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                                                                                                                                           94WO-0SGC500.
                                                                                                                                                                                         93US-0123343
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Best Local Similarity 49.1
Matches 104; Conservative
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                                              /*tag=
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P-PSDB; AAR55791.
                                                                                                                                           14-JAN-1994;
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                                                                           W09416071-A.
                                                                                                           21-JUL-1994
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ABL08913/c
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Myers EW;

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23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                              23-MAR-2001; 2001WO-US09231
                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                        WPI: 2001-656860/75
                                                                                                         (PEKE ) PE CORP NY
                                                                                                                                                                     P-PSDB; ABB64809
W0260171642-A2.
                                                                                                                                                                                                                     interactions
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                        27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 AACCCACAAAACGGACCGATCATGGCGCGGGGGAAAGGTGATGTGCTCGCTGTC 439
                                                                                                                                                                                                                                                                                           v:
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                                                                                                                                                                                                                                                                                                                                                                                     specification, but was obtained in electronic format directly from WIPC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                    genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                           The invention relates to an isolated mucleic acid detection reagent capable of detecting 1000 or more genes from Tycsophila. The invention useful in developmental biology and in elucidating cell signalling and call-cell interactions in higher cukaryotes for the development of inscetticides, thorapeutics and pharmaceutical frugs. The invention discloses genomic DNA sequences (ABLD1676 ABL3551), expressed DNA sequences (ABLD1840-ABL16175) and the encoded proteins
                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                              (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEG ID NO 21218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.7%; Score 39.2; DB 23; Length 3988; 49.1%; Pred. No. 0.11;
                                                                                                                                                                                                                                                      Claim 1; SEG 1D NO 21221; 21pp + Sequence Listing: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3988 BP; 1316 A; 893 C; 753 G; 1026 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1365 GIACTCGCGCTCATCCTCGCCGTCGAGGTCA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500 TATATCGAATCCATGTTGCCCCGGGGGGTTGA 531
                                                                                                                                              Myers EW:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL08912 stundard; cDNA; 19867
                                                                                                                                              PWI),
                                                           23-MAR-2001; 2001WO-US09231.
                                                                                  23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                                   WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                      (PEKE ) PE CORP NY
                                                                                                                                                                                P-PSDB; ABB64810.
           W0200171642-A2
                                                                                                                                                                                                                                interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104:
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                                   27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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ABL08912/c
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14336 GGCCGTAAAGTTGTCGTAGCGATCGCCAAACTCGTCCCAAGTGGCCTCATGATGGTTGTTG 14277
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                                                                                                                                                                                                                                                                      1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 ACACCCGTCCTGACCATCGAACCCGGTGACCGGAITATTGTCGACACTCGAGATGCTTII 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AAUCCACAAAACGGACCGATCATGGTCAATGGCGCGGGAGAAGGTGATGTGCTCGCTGTC 499
                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention usert, in developmental biology and in elucidaring cell signalling and cell cell circlel interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL30511), and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
New isolated nucleic acid detection reagent for detecting 1000 or more quees from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis; Neisseria gonorrheae; genome; immumogenic;
antigen: vaccine; diagnosis; infection; antibacterial; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 GAAGGTGCTATCAATTGGGAACAGGATATTCCGAGCCAGTTGCTAAAAATGCCCTTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14396 GGAGCTCTTCTTCTGGGGGGGGGATGCGTCCATTGAACTCCTGCAGACGCTCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 19867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19867 BP; 6006 A; 3967 C; 3859 G; 6035 T; 0 other;
                                                                                                                                                       Claim 1; SEQ ID NO 21218; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N. meningitidis partial DNA sequence gnm_25 SEQ ID NO:25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.7%; Score 39.2; DB 23;
49.1%; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14276 GTACTCGCGCTCATCCTCGCCGTCGAGGTCA 14245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATATCGAATCCAIGTTGCCCCCCCCCCCGCGTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Sest Local Similarity 49.1%
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meningococcus B; MenB; ds
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(first entry)

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13-MAR-2001
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                                                                                                                                                                                              23055 GCATCTIANACAAAAAACAGGCAAAAAGCIATGATGACGGAAAGGCGAGTTTATGGGGGGG 22995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22995 AGGGAAGCATTATTIGAACACATCGAAGACCAAATCGACGAAAACGGCIGGGAIITTGGAC 22936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 GAATAACATATGAAATGGTTGGAAGAATCCATTATGGCCAAACGCGGTGTTGGTGCCGGG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 CGTAAACCGGTAACGCATCACCTGACGGAAGAAATGCAAAAAGAGTTTCATTACACCATT 307
                                                                                                                                                                                                                                                                                                                                                                Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.
                                                                                             4, Venter JC;
Scarselli M, Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                               Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                           2.7%; Score 39.2; DB 21; Length 25778; 52.4%; Pred. No. 0.37; tive 0: Mismatches 78; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22935 TGCCGGTTTGCCGGAAACGTCCTGACCATCGAAGCCGGAGAGG 22892
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26778 BP; 6602 A; 7008 C; 6846 G; 6318 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 GCCCTTATTCCACACCCGTCCTGACCATCGAACCCGGTGACCG 351
                                                                                             Tettelin H,
Ratti G, Sc
                                                                                                                                                                                  Claim 7; Page 524-531; 1760pp; English
                                                                                             ickey E, Peterson J,
Galeotti C, Mora M,
                                  99W0-0S23573.
                                                  9805-0103794
9905-0132068
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 52.4
86; Conservative
                                                                                             Hickey E.
                                                                                                     Masignani V, Galeott
Rappuoli R, Pizza M;
                                                                            (CHIR ) CHIRON CORP.
                                                                                                                                WPI; 2000-318079/27
WO200022430-A2
                                                          30-APR-1999;
                                  08-OCT-1999;
                 20-APR-2000
                                                                                            Frazer CM,
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Best Local S
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AAF21612 standard; DNA; 349960 BP.

AAF21612;

AX A

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The present invention describes the full length genome of
Neisseria meningitidis B (NMB). The sequences in AAP21544 and AAF21607
C Neisseria meningitidis B (NMB). The sequences in AAP21544 and AAF21607
c to AAP21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into B sequences which overiap each other at the beginning and end of each sequence by 49800 bp (i.e. the last 49980 bp of AAF2164 is repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21607 are repeated at the beginning of AAF21608, and so on). AAF21545 to AAF2168 encode the Noisseria proteins given in AAB38550 to AAB28593, and AAF2158 encode the Noisseria proteins given in AAB38550 to AAB28593, and AAF2158 to the present invention. The NMB genome and fragments from it have antipacterial activity, and can be used in vaccines and gene therapy.

Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection of the Neisserial bacteria or of antibodies which binds to the proteins conputers. Computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide turther opportunities to find antipodies immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276041 AGCGAAGCATTATTTGAAGACATCGAAGACCAAATCGACAAAAGGGGTGGGATTTCGAC 276100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masignani V:
Rappuoli R;
                                                                                 Noisseria meningitidis; Neisseria gonorrheae; immunogenio; vaccine;
diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections \cdot
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Neisserla meningitidis B nucleotide sequence SEQ ID NO:113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
Scarlato V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 GGCCCTTATTCCACACCGTCCTGACCATCGAACCCGGTGACCG 351
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Scarselli M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-1999; 99US-0132068.
08-0CI-1999; 99WO-US23573.
28-PEH-2000; 2000GB-0004695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2000; 2000WO-US05928.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                              Neisseria meningitidis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pizza M, Hickey E,
Galcotti C, Mora M,
Frazer CM, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-647603/62
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Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                               WO200066791-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2000
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Gaps

.; 0

Indels

78;

0; Mismatches

86; Conservative

Matches

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The present invention describes methods of obtaining immunisciic proteins from Neisseria genomic sequences. AAA81451 squence: 0.NA represent specifically claimed Neisseria monimitidis squence: 0.NA sequences. AAA81250 to AAA81363 to AAA81360 to AAA81560 to AAA81560 to AAA81560 to AAA81560 to AAA81560 to AAA81560 to Cresponding proteins. AAA81254 to AAA81259 and AAA81361 represent Pork primers used in the collection of Neisseria meningitidis bNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis Menb polyncolectide ORF sequences, which are all used in the exemplification of the present of any analysis of a composition. The composition can be used in the manufacture of a composition can be used as a medicament (or in the manufacture of a composition can be used as a medicament (or in the manufacture of a composition of treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all assorbypes; and/or against all pathogenic Neisserial of form the manufacture of a components of vaccines against Meningococcus B; against all serotypes; cand/or against all pathogenic Neisserial of Delugical probes; confirm will also facilitate production of sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scarlate V:
                                                                                                                                                                                                                                                                                                    Neisseria meningitidis; Neisseria gonorrheae, gonome: immunogenic;
antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly organism specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolcrance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, compicte sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleotide sequences of Neisseria meningitidis which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonerrheea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 837096 BP: 207534 A; 227065 C; 205215 G; 197280 T; 2 other;
Tettelin H, Venter JC:
Ratti G, Scarselli M.
                                                                                                                                                                                                                                                            N. meningitidis partial DNA sequence gnm_37 SEQ 1D NC:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7: Page 629-865; 1750pp: English.
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C, Mora M,
                                                                                                                                BP
                                                                                                                                AAA81489 standard; DNA; 837096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US23573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other more variable regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0103794.
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hickey E, F
                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis
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Masignani V. Galeceurais R. Pizza M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200022430-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-1999;
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                                                                                                                                                                        AAA81489;
                                                                                                         AAA81489
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Score 39.2; DB 21; Length 837096; Pred. No. 3.3;

2.78;

Ouery Match Best Local Similarity

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643752 GCAICTTAAACAAAAAACACGCAAAAAGCIATGAIGACGGAAAGGGAGITTATCCGCGCG 640811
                                                                            .
0
188 GAATAACATATGAAATGGTTGGAAGAATCCATTATGGCCAAACGCGGTGTTGGTGCCGGG 247
                                                          248 CGIAAACCGGTAACGCATCACCTGACGGAAGAATGCAAAAAGAGTTTCATTACACCATT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The reaper (rpt) and head involution defective (hid) genes, mapping to position 75C1.2 of D. melanogaster chromosome 3, exhibit coxpicssion patterns related to the pattern of cell death during broscophila embryogenesis. Cell death genes, or antisense sequences, can be used to reduce or abblish apoptosis, e.g. in transgenic animals. The genomic sequence of hid is given as 4 contiguous sequences in AAQ66946-49, which together encode HID protein.
                                                                                                                                                                                                                                                                                                                                            Cell death; head involution defective; hid gene; reaper gene; rpr; apoptosis; transgenic animal; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isclated cell death genes from Drosophila - and novel assays for appoptotic cell deaths and apoptotic and necrotic cell deaths, based on selective staining by toluidine blue, acridine orange and Nile blue
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"Base n at position 93 is not identified
in the specification"
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                                                                                                                                     308 GGCCTTATICCACACCGTCCTGACCAICGAACCCGGTGACCG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 502 BP; 141 A; 135 C; 135 G; 90 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             White
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                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                          AAQ66948 standard; DNA; 502
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Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
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                                                                                                                                                                  440 AACCCACAAAACGGACCGATCATSGTCAATGGCGCGGAGAAAGGTGATGTGCTCGCTGTC 499
                                                                                                                                                                                                      939 GGCCGTAAAGTTGTCGTAGCGATCGCCAAACTCGTCCCAAGTGGCCTCATGATCGCTCTG 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition, useful in screening assays for antagonists and agonists of Hid phosphorylation by mitogen activated protein kinase (MAPK), comprises DNA having an oligonucleotide sequence of mutant forms of the Droscphila hid gene
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                                                                                                             ACACCCGTCCTGACCATCGAACCCGGTGACCGGATTATTGTCGACACTCGAGATGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hid; mitogen activated protein kinase p42/p44; phorylation; apoptosis; ss.
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/label= wild type A G replaced with G C
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//abel= Wild type A replaced with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster hidala3 cDNA.
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/label- Wild type A
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/product= HidAla3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphorylation; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                              дH
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               320
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AAA27103/c
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                   380 GAAGGIGGTATCAAIICGGAACAGGATAIICGGAGGCAGIWGGIAAAAAIWGCGIITGIG 439
                                                                                                                                                  440 AACCCACAAAAGGGACCGATOATGGTCAATGGCGCGGGGGAAAGGTGATGTSCTCGCTGTC 499
                                                                                                                                                                        homologs
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320 ACACCCGTCCTGACCATCGAACCCGGTGACCGGGATTATTGTCGACACTCGAGATGCTTTT
                                                                                               2.6%; Score 37.6; DB 21; Length 1233; 48.6%; Pred, No. 0.18;
tive 0; Mismatches 109; indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fruit fly; Hid: mitogen activated protein kinase p42/p44;
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                                                                                                                                                                                                                                                               153 GTACTCGGGCTCATGCTCGGGGGGGGGGGGGTCA 122
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99US-0431573
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Best Local Similarity 48.6
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                    GAAGGTGCTATCAATTCGGAACAGGATATTCCGAGCCAGTTGCTAAAAATGCCCTTTGTC 439
                                                                                                                                                                                                                                                                                                                                                                              440 AACCCACAAAAGGGACCGATCATGGTCAATGGCGCGGAGAAAGGTGATGTGTGCTGTTTT 499
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 thought to inhibit Hid induced cell death. Mutant forms of the hid
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                                                                                                                                                                                                  tch 2.6%; Score 37.6; DB 21; Longth 1233; al Similarity 48.6%; Pred. No. 0.18; 103; Conservative 0; Mismatches 109; Indels 0;
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/Jabel- Wild type A replaced with G
751.752
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/label- wild type A G replaced with G C
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                                                                                                                                                                          Sequence 1233 BP: 247 A: 453 C: 330 G: 203 T: 0 other;
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|abel= Wild type A replaced
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'label= wild type A G
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Best Local S
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AAA27104/C
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                                                                                                                                                                                                                                                                                                                                                         The product of the Drosophila melanogaster hid gene is responsible for inducing apoptosis in embryos. Activation of the Ras/MAPK pathway is thought to inhibit Hid induced ceil death. Mutant forms of the hid gene, hidala3 and hidala5 have been generated in which DNA encoding phosphoacceptor residues is replaced with DNA encoding non-phosphorylatable amino acids. These mutants are not suppressed by KARK induced phosphorylation. Compositions from the mutant gene are useful in screening assays for aniagonists and agonists of Hid phosphorylation: by mitogen activated protein kinase (MAPK). They may also be used to identify new constituents of the Hid signailing pathway. The new compositions may be useful in identifying new homologs of Hid or its natural mutations. The present sequence is the CONA
                                                                                                                                                                                                                                           Composition, useful in screening assays for antagonists and agonists of Hid phosphorylation by mitogen activated protein kinase (MAPK), comprises DNA having an oligonucleotide sequence of mutant forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 GAAGGIGCIATCAATICGGAACAGGATATICCGAGCCAGTFGCTAAAAAIGCCCTTTCIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 AACCCACAAAACGGACCGATCATGGTCAATGGCGCGGAGAAAGGTGATGTGCTCGCTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.6%; Score 37.6; DB 21; Length 1233; 48.5%; Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1233 BP; 245 A; 454 C; 331 G; 203 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 109;
                                                                                                                                                          Bergmann A, McCall K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIACTCGCGCTCAICCTCGCCCGTCGAGGTCA 848
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                                                                                                                       (MASI ) MASSACHUSETTS INST TECHNOLOGY
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                                    99WO-US25514.
                                                                                      99US-0431573
                                                                    98US-01C6108
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                                                                                                                                                              Agapite J,
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P-PSDB: AAY94424.
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                                    29-0CT-1999;
                                                                                        29-0CT-1999;
11-MAY-2000
                                                                     29-0CT-1998
                                                                                                                                                            Steller H,
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176 ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or nore genes from Drosophila and for elucidating cell signalling and cell-cell
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Best Local Similarity 47.8%; Pred. No. 0.8;
Matches 107; Conservative 0; Mismatches 117; Indeis 0;
                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 12502; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                             Myers EW:
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                                                                           23-MAR-2001; 2001WO-US09231.
                                                                                                                23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                             Adams M,
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WC200171042-A2
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                                         27-SEP-2001
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Search completed: July 6, 2003, 05:04:33 Job time : 369 secs

1145 GIGAGCGTGACCGGTICGGCGGCTTAGGGCGTGGCNAAAGTTTTTCCAAATGGATACA 1204

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Searched:

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Sequence Sequence Sequence Sequence

Sequence 45, R Sequence 17, R Sequence 11, R Sequence 2055, Sequence 2055, Sequence 1, R

Seguence 1, Seguence 101

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US-08-123-343A-15/C
Sequence 15, Application US/08123343A
Sequence 15, Application US/08123343A
Sequence 15, Application US/08123343A
Sequence 15, Application
Sequence 15, Application
GENERAL INFORMATION:
APPLICANT Steller, Hermann
APPLICANT Mitte, Kristin
ITTLE OF INVENTION: Cell Death Genes of Drosophila
ITTLE OF INVENTION: Cell Death Genes of Drosophila
ITTLE OF INVENTION: Melanoquater and Vertebrate Analogs
NUMBERS ON SEQUENCES: Melanoquater and Vertebrate Analogs
NUMBERS PROBRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Amiltin Drive
CITY: Lexington
STATE: Ma
COUNTRY: US
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COMPOTER: Floppy disk
COMPOTER: Darbor occupatible
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COMPARE: 17.5EP-1993
COMPARE: 17.5EP-1993
COMPARE: 17.5EP-1993
COMPARE: 15.5AN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGENTATION NUMBER: 32.272
                                                                                                   US-08-822-586-45

US-09-622-015-1

US-09-007-005-17

US-09-007-005-17

US-08-244-706-17

US-08-924-107-1

US-08-485-107-1

US-08-485-107-1

US-09-134-0012-2055

US-08-471-119A-1

US-08-452-915-6

US-08-452-915-6

US-09-134-0012-138
                                    US-08-682-643-1
US-08-998-416-1016
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TYPE: nucleic acid
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Bost Local Similarity 48.6
Matches 103; Conservative
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'cqn2_6/ptoda=x1/ina/6A_COMB.seq:*
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6: /cqn2_6/ptoda=x1/ina/ptoTUS_COMB.seq:*
                                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-056-200-93
US-08-060-644-93
US-08-374-686-1
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US-08-943-731-193
US-08-943-731-5
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US-06-633-770A-11
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Maximum Match 160%
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Maximum DB seq length: 200000000
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Perfect score:
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TITLE OF INVENTION: INHIBIT MAPK MEDIATED ANTI-AFOPTOTIC SIGNALS
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48.6%; Pred. No. 0.035;
tive 0; Mismatches 109; Indels
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            CURRENT APPLICATION NUMBER: US/05/431,573
CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 65/106,108
PRIOR FILING DATE: 1998-10-29
NUMBER: FELING DATE: 1998-10-29
SOFTWARE: Patentin Ver: 2:0
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Patent No. 6235524
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39-431-573-3
                                                                                                                                                                                                         ) OKGANISK: Drosophila melanogaster
US-09-431-573-2
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Matches 193; Conservative
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GENERAL INFORMATION:
APPLICANT: STELLER, HERMAN
APPLICANT: ACAPITE, JULIE
APPLICANT: MC CALL, KIMBERLY
APPLICANT: BERGMANN, ANDREAS
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING AGENTS THAT
TITLE OF INVENTION: INHIBIT MAPK MEDIATED ANTI-APOPTOTIC SIGNALS
FILE REFERENCE: MIT-04019
CURRENT PELING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: GC/106,108
PRIOR FILING DATE: 1999-10-29
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Patent No. 6235524
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APPLICANT: AGAPITE, JULIF
APPLICANT: MC CALL, KIMBERLY
APPLICANT: BERGMAN, AMDREAS
TITLE OF INVENTION: COMPOSIT
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Best Local Similarity 48.6
Matches 103; Conservative
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GENERAL INFORMATION:
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US-09-431-573-1/c
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SEQ ID NO
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320 ACACCCGTCCTGACCATCGAACCCGGTGACCGGATTATTGTGGACACTCGAGATGCTTTT 379
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APPLICANT: AGAPITE, JULIE
APPLICANT: MC CALL, KIMBERLS
APPLICANT: MC CALL, KIMBERLS
APPLICANT: BERGHANN, ANDREAS
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING AGENTS THAT
ITLE OF INVENTION: UNHIBIT MAPK MEDIATED ANTI-APOPTOTIC SIGNALS
FILE REFERENCE: MIT-04019
CURRENT APPLICATION NUMBER: US/09/431,573
CURRENT APPLICATION NUMBER: US/09/431,573
CURRENT APPLICATION NUMBER: 00/106,108
PRICR FILING DATE: 1998-10-29
NUMBER: OF SEC ID NOS: 5
SCFTWARE: PALCALIN VET. 2.6
SEC ID NO 3
                                                                          Gaps
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2.6%; Score 37.6; DB 4; Length 1233; 48.6%; Pred. No. 0.035; 1ive 0; Mismatches 109; Indels 0
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939 GGCCGTAAAGITGTCGTAGCGATCGCCAAACICGTCCAAGTGGCCTCATGAICGCTCTG 880

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1224 GGGGTAATGIGIAAGTICAAACAATGGCTATTTTTAACAGCTAAAG 1269
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APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Clark, Steven E.
ITTLE OF INVENTION: Plant Clavatal Nucleic Acids,
ITTLE OF INVENTION: Transformed Plants, and Proteins
NUMBAGE OF SEQUENCES: 11
CORRESPONDENCE FADRESS:
ADDRESSE: Flext, Hoibach, Tost, Albritton & Horbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDCIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURKNIT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35.2; DB 4;
Pred. No. 0.12;
                                                                               GENERAL INFORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
CONTRIBUTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR APPLICATION NUMBER: 60/058,612
NUMBER OF SEQ. ID NOS: 58
SOFTWARE: FARLSEQ for Windows Version 3.0
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-60886/RET/RMS
IELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 731-1989
TELEPAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                     US-09-144-367-7/c
; Sequence 7, Application US/09144367
; Patent No. 6432639
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Best Local Similarity 57.5%;
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C.T.San Francisco
STATE: California
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ORGANISM: H. sapiens
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US-09-144-367-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Other
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US-08-473-553A-1
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                                                                                                                                                                                                                        APPLICANT: Steller, Herman:
APPLICANT: Steller, John M.
APPLICANT: Abrams, John M.
APPLICANT: White, Kristin
TITLE OF INVENTION: Cel. Death Genes of Drosophila
TITLE OF INVENTION: Melanogaster and Vertebrate Analogs
NUMBER OF SEQUENCES: 16
CORRESSORE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Fwo Militan Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1278 Gracicgesercarceresecesterassica 1247
500 TATATCGAATCCATGTTGCCCCGCGCGTTGA 531
                               111 | 1 | 1 | 879 GTACTCGCCCGTCGAGGTCA 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSITION NUMBER: US/08/123,343A
FILING DATE: 17-SEP-1993
CLASSITICATION: 806
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,957
FILING DATE: 15-JAN 1993
ATJORNORY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5907A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            Sequence 6, Application US/08123343A Patent No. 5593879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 61861-9540
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3900 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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STREET: Two ...
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                                                                                                                                      US-08-123-343A-6/C
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                                                                                                              RESULT 5
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315 ACACATATCTTCAAATGTACTACAAATCACTGAACTGTATATTTTAAGTGGATGAATTAC 256
                                                                   1164 ACAAAAACCISTTAGIITAGFAGGAATAACTAACCGGTGAACATTACCGGGATGTAGATC
Gaps
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APPLICANT: Yu, Shukun
APPLICANT: Kragi, Karsten
APPLICANT: Kragi, Karsten
APPLICANT: Christensen, Tove
APPLICANT: Christensen, Jan
TITLE OF INVENTION: ALPHA-1.4-GLUCAN LYASE PROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   303 CCATIGGCCCITATTCCACACCCGICCTGACCATCGAACCCGGIGACCGGATTATTGTCG 362
                                                                                                                                                                                                                                                                                                                                                                                                    2.3%; Score 33.2; DB 2; Leigth 3201; 50.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 ACACTCGAGATGCTTTTGAAGGTGCTATCAATTCGGAACAGGATAT 408
                                                                                                                                                                                                                                                 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OFFRATING SYSTEM: DOS
OFFRATING SYSTEM: DOS
OFFRATING SYSTEM: DAS
OFFRATING APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
SIATE: CA
                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYOUG. 001APC
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FILIUS DATE: July 8, 1996
FLICASIPICATION: 435
PRICK APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08633770A
Patent No. 590870
GENERAL INFORMATION:
APPLICANT: Bojsen, Kirsten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34,115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEC ID NO: 11:
SECUENCE CHARACTERISTICS:
LENGTH: 4726 base pairs
                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
         INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3201 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                             Bost Local Similarity 50.0
Matches 83, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 714-760-04
TELEFAX: 714-760-9502
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STRANDEDNESS: single
                                                                                                   double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                              STRANDEDNESS:
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US-08-633-770A-11/c
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APPLICANT: Yu, Shukun
APPLICANT: Yu, Shukun
APPLICANT: Yraqh, Karsten
APPLICANT: Christensen, Tove
APPLICANT: Marcussee, Jan
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, 1TS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICRORGANISMS
CORRESPONDENCE ALD ALPHESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        1136 CCCAAATACACCGTTGGCGCGATGCTGAACAAAACCTGTTAGTTTAGTAGGAATAACTA 7195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1256 TTTAACAGCTAAAAGCAGGTGCATATGGGGCCAGATACACCCATCAAT 1302
                                                                                                                                                                                                                                                                                                                                                         DB 2: Length 5733;
                                                                                                                                                                                                                                                                                                                                                       Query Match 2.4%; Score 34.2; DB 2; Length 5 Best Local Similarity 50.3%; Pred. No. 1.2; Matches 84; Conservative 6; Mismatches 85; Indels
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SOFTWARE: Patentin Releasn #1.0, Version #1.25 (RFO)
CURRENT APPLICATION DATA:
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620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Altman, Daniel E
REGIGTRATION NUMBER: 34,115
REFERNCE/DOCKET NUMBER: DYCU6.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0464
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FILING DATE: CCT-15-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/533,770A
FILING DATE: July 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08633770A Patent No. 5903760 GENERAL INFORMATION:
                                                                                                                                                              MCLEGULE TYPE: DNA (genomic)
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
                                                                                              TYPE: nucleic acid
STRANDEDNESS: unknown
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MEDIUM IYPE: Diskett
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STATE: CA
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                                                                                                                                                                                                         NAME/KEY: CDS
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TELEX:
                                                                                                                                                                                                                                                                      NAME/KEY:
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US-08-473-553A-1
                                                                                                                                            TOPOLOGY:
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                                                                                             243 CCGGGCGTAAACCGGTAACGCATCACCTGACGGAAGAAATGCAAAAAAGAGTTTCATTAGA 302
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                                                                 Gaps
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                             2.3%; Score 33.2; DB 2; Length 4726; 50.0%; Pred. No. 2.4; tive 0; Mismatches 83; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7218;
                                                                                                                                                                                                                                        363 ACACTCGAGATGCTTTTGAAGGTGCTATCAATTCGGAACAGGATAT 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: ISM FC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin RClease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FAIKNER, F. G.
IIILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)835-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: APPLICATION NUMBER: EP 91 114 300.
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PRICK APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 05/05/232,463
                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 193;
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACIERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-AUG-1991
AITORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRAIION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.3%;
Best Local Similarity 3.5%;
Matches 13; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 7218 base pairs
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                             Query Match 2.3 Best Local Similarity 50.0 Matches 83; Conservative
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US-08-232-463-14
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US-08-633-770A-11
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CITY: AL
STATE: V
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1051 GGTAGAAGACITIGGCTICGAACAAIGGGATGCCIACAIGCTTCIGAGTCAAIGCGGCAA 1110

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1231 TGTGTAAGTTCAAACAATCGCTATTTTAACAGCTAAAAGCAGGTGCATATGGGGCCAGAT 1290
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                                                                                                                                                                                                                                                                                                                                                                                                                                     426 AAATGCCCTTTCTCAACCCACAAAAGGGACCGATCATGGTCAATGGCGGGGAGAAAGGTG 485
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                                                                           1111 AGTGGGGTGGGGAAGATGGTGGACCCCAAATACACGGTTGGGGGGATGCTGAACAAAA
                                                                                                                           1171 CCTGTTAGTTTAGTAGGAATAACTAACCGGTGAACATTACCCGGATGTAGATCGGGGTAA
                                                                                                                                                                                                                                                                                                                               1351 TCACAATGGCGCGGAGCAACCCAGGCTATTGCCGAAATTAATCAAAATGGCGGCATCAAC
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APPLICANT: Heinrich-Pette-Institut
SITUE OF THYNENTON:
ELLE GEFERENCE: P50489
CURRENT APPLICATION NUMBER: US/05/309,572
CURRENT APPLICATION NUMBER: US/05/310
EARLIER APPLICATION NUMBER: UE 1994-05-11
EARLIER APPLICATION NUMBER: UE 1995 56 463
EARLIER FILING DATE: 1998-11-26
NUMBER CF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Lymphocytic charlomeningitis virus
08-09-309-572-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09309572
Patent No. 6440730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steinert, Peter
Lee, Seung-Chul
Kim, In-Gyu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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APPLICANT: Chung, Soo-11
APPLICANT: Park, Sang-Chul
TILLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TILLE OF INVENTION: Mehods of Using Same
CORRESPONDENCE: 117
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOIHETICAL: N
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                92660
                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION:
US-08-800-644-93
                                                                                                                                                                                                                 COUNTRY
                                                                                                                                                                        CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3064 CGAGAGCCCAAGACAGAGGTTCCAGGAGGAAGAAGAAGAGAGGAGGAAGCGCGAG 3123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3124 ACAGTGCTCCGGAAGAAGAAGAAGTTGCAGGAAGAGGGGCCCCAAGCGCAAAGAAGAAGA 3183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GCACAGCGCTGTGCGGTAATGGATAAAGGCCTGGTTGTAGAAAGGCTGACCCAACAACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CGGGAACICCATGIGGCCGTGATCCTGGTCGAGCAGGATAIIGCGAIGAIGCAGGGGCC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caps
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APPLICANT: Chung, Soo-Il
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
NUMBER OF SEQUENCES: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 CTCTCTGATGATCTTTTAATGGGTGGTCATCTGGGTCTGTAA 164
                                                                                               CORRESPONDENCE ADDRESS:
CADDRESSEE: Knobbe, Martems, Olson & Bear
STREET: 620 Newport Center Drive, Sixteemily Floor
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/056,200
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fedrick, Michael F.
REGISTRATION NURBER: 36,799
REGISTRATION NURBER: NIH054.001A
FELERANULCATION INFORMATION:
TELEPHONE: (714) 760-0404
TELEPA: (714) 760-0502
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-800-644-93
: Sequence 93. Application US/088C0644
: Pattent No. 5958752
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 9551 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
2512..8070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1645..2511
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                                                                                                                                                                 Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                             U.S.A.
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FEATURE:
                                                                                                                                                                                                                              92660
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
; LOCATION:
US-08-056-200-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                           COUNTRY:
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63 GCACAGCGCTGTGCGGTAATGGATAAAGGCCTGGTTGTAGAAACGCTGACCAACAACAG
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                                                                                                                                                 COMPUTER: TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OFFWARTING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Rolease #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 14-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US C8/056,200
FILING DATE: 30-APR-1993
ATIORNEY/AGENI INFORMATION:
E: Knobbe, Martens, Olson & Bear
62G Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 2.2%: Score 32.4; DB 2; I Hest Local Similarity 50.0%; Pred. No. 6.7; Matches 81; Conservative 0; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: NIHU54.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-374-686-4/C
Sequence 4. Application US/08374686
Patent No. 5616474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEDOMACNICATION INFORMATION:
TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9551 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fedrick, Michael F. REGISTRATION NUMBER: 36,799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
1507..1644
                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
2512..8070
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                                           Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT: Steinert, Peter M. APPLICANT: Lee, Seung-Chul APPLICANT: Kim, In-Gyu

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Search completed: July 6, 2003, 06:42:25
Job time : 108 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gars
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Facer No. 5616474
GENERA: INFORMATION:
APPLICANT: BOICIN, Monique
APPLICANT: Menart, Sandrine
TITLE OF INVENTION: K. lactis Transaldolase Gene Promoter
TITLE OF INVENTION: and Use Thereof
NUMBER OF SEQUENCES: 5
CORRESPENDENCE ADDRESS:
SOORESEE: Rhone-Poulenc Rorer Inc.
SIRRET: 500 Arcola Rd. 3C43
APPLICANT: Bolotin, Monique
APPLICANT: Menart, Sandrine
TITLE OF INVENTION: K. lactis Transaldolase Gene Promoter
TITLE OF INVENTION: and Use Thereot
UNBBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; indeis
                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCI/FR93/60771
FILING DATE: 28-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/09432
ATORNEY/AGENT INFORMATION:
NAME: Smith, Calie K.
REGISTRATION NUMBER: 38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: $792048-US TELECOMMUNICATION INFORMATION: TELEPHONE: (610)454-3839
                                                                                                                        ADDRESSEE: Rhone-Poulenc Rorer Inc
STREET: 500 Arcola Rd. 3C43
                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1220 GATCGGGGTAATGTGTA 1236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1226 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 500 m. TTY: Collegeville
                                                                                                                                                            Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                            19002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                    STATE: P. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                           STREET:
CITY: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-374-686-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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1160 CTGAACAAAAACCTGTTAGTTAGTAGGAATAACTAACGGTGAACATTACCCGGATGTA 1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 2.2%; Score 32.2; DB 1; Length 1349;
Bost Local Similarity 63.6%; Pred. No. 2.3;
Matches 49; Conservative 0; Mismatches 28; Indels 0
                     MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSIEM: PT-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,686
                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
TFILING DATE: 28-7UL-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: W. PCT/FR93/00771
FILING DATE: 38-7UL-1993
APPLICATION NUMBER: FX 92/09432
FILING JATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
RECISTRATION NUMBER: 38,619
REPERBENCE/DOCKET NUMBER: ST92048-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFRAX: (610)454-3839
INFORMATION FOR SEO 1D NO: 1:
SEQUENCE CHARACTERISTICS:
TENTIFY: TANTH': 1349 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Kluyveromydes ladtis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1220 GATCGGGGTAATGTGTA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 GATGGAGCTATATTTA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : FOCATION: 1297..1347
US-08-374-686-1
COMPUTER READABLE FORM:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 6, 2003, 06:07:31; Search time 273 Seconds (without alignments) 8245.237 Million ceil updates/sec Run cn:

US-10-086-082-1 Title: Perfect score:

1 eccgggaactecatgtggcc.....aatgcaatteatttggatec 1442 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

1085931 scqs, 780495707 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq.length: C Maximum DB seq.length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_NA:* Database

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10:

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SUMMARIES

	Description	Sequence 1. Appli	Sequence 88, Appl	Sequence 411, App	Sequence 464, App	Sequence 7. Appli	Sequence 60, Appl	Sequence 310, App	Sequence 310, App	Sequence 14. App)	Sequence 123. App	Sequence 372, App	Sequence 3151. Ap	Sequence 6010. Ap	Segmence 1, Appli	Sequence 2052. Ap	Sequence 2327. An	Sequence 346. App	Segmence 346. App	
	Ω	US-10-086-082-1	US-10-108-605-88	US-09-770-444-411	US-10-123-155-464	US-10-146-575-7	US-10-123-155-60	US-10-184-644-310	US-1C-184-634-310	US-10-C27-828-14	US-10-153-668-123	US-09-833-381-372	US-09-738-626-3151	US-09-815-242-6010	US-09-738-626-1	US-09-983-965-2052	US-09-983-965-2327	US-10-184-644-346	US-10-184-634-346	US-10-123-155-358
	55	- 6	5	10	6	6	တ	6	σ.	2	σ	10	6	10	6	10	10	o	σ	σ
	Query Match Length DB	1442	3902	461	941	429	724	296	596	3198	4153	481	1068	1839	3309400	284	415	671	67;	1049
æ	Query Match	100.0	2.6	2.5	2.5	2.4	2.4	2.4	2.4	2.4	2.4	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3
	Score	1442	37.6	36.2	35.8	35.2	35	34.4	34.4	34.2	34	33.8	33.8	33.8	33.8	33.6	33.2	33.2	33.2	33.2
	uìt No.		7	Ŋ	4	S	9	7	œ	ù	10	11	12	13	14	15	16	17	18	19
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05 12 13 14 14 15 16 17 17 18 17 18 18 18 18 18 18 18 18 18 18	sequence 135, App Sequence 135, App Sequence 117, App Sequence 6205, Ap Sequence 22134, App Sequence 204, App Sequence 204, App Sequence 43, App Sequence 283, App Sequence 983, App
	18.09.25.299.135 US. 09-925-299-135 US.10-156-76.1 US.10-156-76.1 US.10-156-76.1 US.09-918-995-22134 US.10-184-644-204 US.10-184-644-204 US.10-060-036-43 US.10-153-668-283
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APPLICANT: Maughton, Mailer
APPLICANT: Naughton, Andrew
APPLICANT: Naughton, Andrew
APPLICANT: Shaw, Nicholas
APPLICANT: Shaw, Nicholas
APPLICANT: Zhaw, Nicholas
APPLICANT: Zhaw, Nicholas
APPLICANT: Zhaw, Nicholas
APPLICANT: Zhamermann, Thomas
THILE OF INVENTION: METHOD OF PREPARING (S)-OR (R)
THILE OF INVENTION: -5.3,3-TRIFLUCNO-2-HYDROXY-2-METHYLPHOPIONIC ACID
FILE REFERENCE: 32213
CURRENT APPLICATION NUMBER: 105/10/086,082
CURRENT APPLICATION NUMBER: 105/09/214,679
PRIOR PRIOR APPLICATION NUMBER: US/09/214,679
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 24
SOPTWARE: FastSEC for Windows Version 3.0
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100.0%; Pred. No. 0;
tive 0; Mismatches
                    Sequence 1, Application US/10086082
Publication No. US20030087402A1
                                                                                                                                                                                                                                                                                                                                                                                                               / TYPE: DNA
/ ORGANISM: Klebsiella oxytoca
US-16-086-082-1
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Bost Local Similarity 100.0
Matches 1442; Conservative
                                                       GENERAL, INFORMATION:
APPLICANT: Bricdon, Walter
APPLICANT: Naughton, Andre
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US-10-086-082-1
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APPLICANT: Broadus, Julie
APPLICANT: Stam. Lynn
APPLICANT: Stam. Lynn
APPLICANT: Stam. Lynn
APPLICANT: Stam. Lynn
APPLICANT: Wandar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOR
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILLE REPERENCE: 31138
CURRENT FILLING DATE: 2002-03-27
PRIOR PILLING DATE: 2001-01-16
PRIOR FILLING DATE: 2001-01-16
                                                                                                      1321 IICAGCGGAGTGACGGCGCACAAGAGTTGTCACAATGCCGCGGAGCAACCCAGGCIATT 1380
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                           GCCGAAATTAATCAAAATGGCGGCATCAACGGCAGACCACTCAATGCAATTCATTTGGAT 1440
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     Gaps
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PRIOR FILING DATE: 2000-01-14
NUMBER OS SEQ 1D NOS: 361
SOFTWARE: Patentin Ver: 2.1
SEO ID NO 88
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Patent No. US20620023280A1
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Patent No. US20020160934A1
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CRGANISM: Drosophila melanogaster
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APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Clang
APPLICANT: Hamilton, Caro: M.
APPLICANT: Frice, Jennifer L.
APPLICANT: Raines, Tracy M.
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GENERAL INFORMATION:
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| CC | 1442
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US-10-108-605-88/c
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                                                                                                      TGCCGGGGGTAAACCGGTAACGCATCACCTGACGCAAGAAATGCAAAAAGAGTTTCATTA 300
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ACIDS ENCODING THE SAME
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TITLE OF INVENTION: ACIDS FILE REFERENCE: P3330R1C30
                                                                                                                                                            ; CRGANISM: Homo Sapien
US-10-123-155-464
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US-10-146-575-7/C
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 GCCGGGCGTAAACCGGTAACGCATCACCTGACGGAASAAAT 282
                                                                                                                                                                                                                            APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Labaliana
FILE REFERENCE: 2027 (PARA-015PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
PRIOR TELING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 36.2; DB 10;
50.7%; Pred. No. 0.23;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 464, Application US/10:23155
Publication No. US20030668794A1
GENERAL INFORMATION.
APPLICANT: Baxer, Kevin P.
APPLICANT: Beresini, Marreen
APPLICANT: Deforge, Laura
APPLICANT: Deforge, Laura
APPLICANT: Deforge, Laura
                               Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Weessoor, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                              : TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-411
                                                                                                                      Garcia, Carlos A.
Kricker, Maja
Slader, Ted
Davis, Keith R.
Allen, Keith
                Rameaka, Joshua G.
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Goddard, Audrey
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
Gac, Wei-Qiang
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Smith, Victoria
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Matches 112; Conservative
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US-10-123-155-464
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943 GCTTTCCTGGCCACGAATGGGAGAATGCCGAAAATATTATGAGTATTGGCAGTGCACGTCC 1002
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CORRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-94-15
FRIOR Application removed - See Palm or File Wrapper NUMBER OF SE0 ID NOS: 550
SEQ ID NO 464
LENGTH: 941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cuery Match 2.5%; Score 35.8; DB 9; 1
Hest Local Similarity 6.2%; Pred. No. 6.51;
Matches 47; Conservative 228; Mismatches 482;
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707 SDSM.SMYYMC.Y5D.CBYTWMMAC.CY.ANMSSA.ST.MMSSCM.S.C.T.CST.ATSS 648
                                                                                                    647 SMYTTM.S..M..H.BAMT.Y...YMSMAYB.B.MRMGMC.TYYS.HB.MR.SCY.TR 588
                                                                                                                                                                                                                                                                                                    527 YCSK.HC..R.CN.N.S.GCYRBRCCABSMCBTDCRTR...BHH.SINDG.MMHRGT.C. 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 H.C. ..CCNDNST. .....BY.SM.HTYSBWK.S.Y.M.BMMH.GSRR.R.M. 288
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                                                                                                                                                                  377 TITGAAGGIGCTAICAATTCGGAACAGGATATICCGAGCCAGTIGCIAAAAAIGCCCTTT 436
                                                                                                                                                                                                                587 TS.RSAT..R..CT.H.T.S...MSDAS..C..TGSAASC.G.H.MMWMMNWYH...TK. 528
                                                                                                                                                                                                                                                               437 CTCAACCCACAAAACGGACCGATCATGGTCAATGGCGGGGGAAAGGTGATGTGCTCGCT 496
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FILE REFERENCE: P34.0FMC1227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT PILING DATE: 2002-06-28
                                                                       317 TCCACACCCGTCCTGACCATGAACCCGGTGACCGGATTATTGTCGACACTCGAGATGCT
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Publication No. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Consoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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APPLICANT:
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APPLICANT: Gao, Wel-Qiang
APPLICANT: Gao, Wel-Qiang
APPLICANT: Garitaen, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Times, Daniel
APPLICANT: Times, Daniel
APPLICANT: Attanabe, Colin K
APPLICANT: Attanabe, Colin K
APPLICANT: Stang, Zemin
APPLICANT: Stang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLERO
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P333081C30
CURRENT APPLICATION NUMBER: US/10/123,155
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Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44: Indels
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ved - See Palm or File Wrapper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35.2; DE 9;
Pred. No. 0.49;
l: Mismatches 44;
                 APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYPAA4
FILE REFERENCE: SEG-12P
CURRENT APPLICATION NUMBER: US/10/146,575
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US/09/144,367
PRIOR FILING DATE: 1998-06-31
NUMBER OF SEQ ID NOS: 58
SOFIWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50, Application US/10123155 Publication No. US26030068794A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.5%:
Matches 61: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker,Kevin P.
APPLICANT: Beresini,Mauri
APPLICANT: DeForge,Laura
APPLICANT: Desnoyers,Luc
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                                                                                                                                                                                                                                                                                                                            ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: Other
) LOCATION: (0)...(0)
US-10-146-575-7
GENERAL INFORMATION:
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US-10-123-155-60/c
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                                                                                                                                                                                                                                                                                  LENGTH: 429
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                                                                                                                                                                                                                                                               SEC ID NO 7
                                                                                                                                                                                                                                                                                                           TYPE: DNA
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ò CC CC 5

Gaps

3

257 GIAACGCATCACCTGACGGAAGAATGCAAAAAAAGTTTCATTACACCATTGGCACTATT 316

Matches

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CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
PRIOR AFPLICATION NUMBER: US 60/293,172
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Sest Local Similarity 51.74
Matches 78; Conservative
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10 NO 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 CSNATANICSSAASS. SNABAS. CSSBASS. SNATAST. SSAASSHSNATASTCSSAASS 4:0
                              589 K.KT.SSB.YYW.WN.SWY.YD.TCDNCCC.C.CDR.CD.DKBTAN.ANY.S.SNYSG. 536
                                                                                                                                                                               349 SNABAS CSSBASS SNATACTCSSAASSHSNATASTCSSAASS SNATASTCSSAASS 290
                                                                            409 SNATASBCSSAASS.SNATASICSSBASS.SNATANTCSSAASS.SNATANTCSS.ASS 350
                                                                                                                                                                                                                                                                                                                                                                                                                           289 SNATASTCSSBASSHSNATASTCSSAASS.SNATACTCNSAAYS.SNATASTCSSAAASS 230
                                                                                                                ..CI..CBTIBBSB.A....W.B.SCC.NI.SBIASTSDSAADKCA.TTACSCISABSS
                                                                                                                                                                                                                               585 ACCIGACGGCCAIGCICAAIGAICCGCIGCCAGAAAAGGIGCGCAIGAIIAAACITCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTCCGAGCCAGITGCIAAAATGCGCTTTCICAACGCAAAAAGGGACGGATGAIGGI
                                                                                                                                                       CGTTGATCCCTACGGCATCTGCGCCATGATTCCGCATTTTGGCGGGACT-GACCGGCACCG
                                                                                                                                                                                                                                                                                                          GIGAAAAGGICTACIGGAGCAAACGCCAIACGCITCCCIATAAACCCCCATA-TTGGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIBES AND MICHELD TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 CAATGCCGCGGAGAAAGGTGATGTGCTCGCTGTTATATCGAATCCATGTTGCCCSGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4%; Score 34.4; DB 9; Length 596; 18.7%; Pred. No. i.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior Application removed - Sec File Wrapper or Palm
NUMBER OF SEQ ID NOS: 512
SEQ ID NO 316
LENGTH: 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               764 AATATGGATGTGCCGGATAIAGGACCAGGGAGTAT 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/184,534 CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 310, Application US/10184634 Publication No. US20030068684A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski, Paul J.
Gurney, Austin L.
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Gondard, Audituy
APPLICANT: Gondard, Audituy
APPLICANT: Gurney, Austin L
APPLICANT: Gurney, Austin L
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabo, Colin
APPLICANT: Lang, Zemin
APPLICANT: Zhang, Zemin
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Smith,Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desnoyers, buc
Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Publication No. US2
GENERAL INFORMATION
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ORGANISM:
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Matches
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APPLICANT: Liderke, Wolfgang
APPLICANT: Liderke, Wolfgang
APPLICANT: Heller, Stefan
APPLICANT: Hudspeth, Albert J.
APPLICANT: Hudspeth, Albert J.
APPLICANT: Eriedman, Ceffrey M.
TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACT
FILE OF INVENTION: IT, AND USES THERBOF
FILE REPERRINGE: 600-1-287N
CURRENT FILING DATE: 2001-10-28
PRICE FILING DATE: 2000-10-26
NUCRENT FILING DATE: 2000-10-26
NUCRENT FILING DATE: 2000-10-26
NUCRENT FILING DATE: 2000-10-36
SOFTWAKE: PATCHILD VETSION 3.1
SEQ. 10, NO. 14
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                                          409 SNATASBCSSAASS.SNATASTCSSBASS.SNATANTCSSAASS.SNATANTCSS.ASS
                                                                                                                                                              585 ACCTGAGGGCCAJGGTCAATGATGGGGTGCCAGAAAAGGTGGGGCATGATTAAACTGGACA
                                                                                                                             GIGAAAAGGICTACIGGAGCAAAGGCATACGCITICCCITAIAAAGGCATA-TIGGCACC
                                                                                                                                                                                                                                                   704 TIGAGCGIAICGCCAGAAATTGACICAAICAATTCACIGACGCCAGACAAICACGGGGG
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Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 73; Indels
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APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, ANIO
APPLICANT: MURAMATSU, Shuji
APPLICANT: ISHIZANA, Kenya
TILCOM INVENTION: STATÉ ACTIVATING Gene
FILE REFERENCE: 1254-0207P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 123, Application US/10153668
Publication No. US20030092616A1
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Publication No. US20030013656A1
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811 GGTACGTGCGCCTGGAGGCCGCCTGTTATTGGTGATGCCCATGCTTGTCAGGGTGATGG 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 64.9%; Pred. No. 2.7;
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE D: INVENTION: Identification of Essential Genes in
TITLE D: INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT PILING DATE: 2301-03-21
FRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Indels
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AFFILGANT: YOKOL, HARUHKO
AFFILGANT: SANOH, ARAHHKO
AFFILGANT: SENOH, ARSHING
AFFILGANT: SENOH, ARSHING
AFFILGANT: SENOH, ARSHING
AFFILGANT: OZAKI, AKIO
TITHE OF INVENTION: NOVEL, POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRICH APPLICATION NUMBER: JP 99/377484
PRICH FILING DATE: 1999-12-5
PRICH FILING DATE: 2000-34-07
PRICH FILING DATE: 3-0
                                                                       136 ITITAATGCGTCGTCATCTGGCTCTGTAA 164
                                                                                                                              52 CGCAACAICCTTACACCCGTGCGCTGTIA 24
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: Sequence 6010, Application US/09815242
: Patent No. US20026061569Al
                                                                                                                                                                                                                                                                          Sequence 3151, Application US/09738626 Publication No. US20020197605A1 SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA OKYNEBACTETIUM GLUTAMICUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Massibock, Robert
APPLICANT: Ohisen, Kari L.
APPLICANT: Zyskind, Judish W.
                                                                                                                                                                                                                                                                                                                                                                                                                     ANDO, SELKO
HAYASHI, MIKIRO
OCHIAL, KEJKO
YOKOL, HAMUHIKO
TATELSHI, NAOKO
SENOH, AKIHIKO
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APPLICANT:
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IIILE OF INVENTION: No. US2020132090Ale: Nucleic Acid and Protein Homologs
File Reference: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT APPLICATION NUMBER: 09/516,448
PRIOR APPLICATION UNBER: 09/516,448
PRIOR APPLICATION UNBER: 2000-02-29
NUMBER OF SEO ID NOS: 2050
SOFTWARE: FastSEO for Windows Version 3.0
LENGTH: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 TATGAAATGGTTGGAAGAATCCATTATGGCCAAACGGGGTGTTGGTGCCGGGCGTGTAAAACC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 GGIAACGCAICACCIGACGGAAGAAIGCAAAAAGAGIITCALTACACCATIGGCCCIIA 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 9; Length 4153;
Pred, No. 5.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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PRICH APPLICATION WURBER: US 66/316,031
PRIOR FILING DATE: 2001-08-3;
PRIOR FILING DATE: 2001-08-3;
PRIOR FILING DATE: 2001-16-12
PRIOR FILING DATE: 2001-16-12
PRIOR PLICATION WURBER: JP 2001-157043
PRIOR PLING DATE: 2001-08-26
PRIOR FILING DATE: 2001-08-30
PRIOR PLING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 372, Application US/0983381 Patent No. US20020132090A1 GENERAL INFORMATION:
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: OTHER INFORMATION: n ~ A.T.C or G
US-09-833-381-372
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Best Local Similarity 52.9%
Matches 73; Conservative
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NAME/KEY: CDS
: LOCATION: (175)..(3024)
US-10-153-668-123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo saplens
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PRIOR APPLICATION NUMBER: 60/205,846
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING FATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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TITLE OF INVENTION: NOVEL PCLYNUCLEOIIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/U9/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PLICATION NUMBER: JP 00/159:62
PRIOR PAPLICATION NUMBER: JP 00/159:62
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09738626 Publication No. US20020197605Al GENERAL INFORMATION:
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APPLICANT: MIZOGOGHI, HIROSHI
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
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ORGANISM: Escherichia coli
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US-09-815-242-6010
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Matches 77; Conserv
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FGLERAL IND. USZOVZUIS/LEUAL

GEGLERAL IND. WASTEDN

APPLICANT: Wastey C.

ITHE OF INVENTION: NUCSEE AND FAT DEPOSITION

ITHE OF INVENTION: NUCSEE AND FAT DEPOSITION

FILE REFERENCE: 37-21(10297)C

CURRENT APPLICATION NUMBER: US/09/983,965

CURRENT APPLICATION NUMBER: US/09/983,965

CURRENT APPLICATION NUMBER: US/09/465,231

PRIOR APPLICATION NUMBER: US/09/465,231

PRIOR ETLING DATE: 1999-12-15

PRIOR FILING DATE: 1998-12-17

NUMBER OF SEC ID NOS: 5912

SEC IS NOS: 202

LENGIN: 284

TYPE: DNA
                                                                                                                           3646798 GGTCCCIGTGCGTGGGAGTGGCGTTTTACCTGGTGATGCCGCTTCTCGCGTGGGTGTTGG 3046739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 AGGCCTGGTTGTAGAAAGGCTGACCCAACAACAGCTGTCTGATGATGTTTAATGCGTGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 TCATCTGGCTCTGTAACTAAACGCTATAAATTACGTGGAGAATAACATAATGAAATGGTTG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 GGICGAGCAGGATAITSCGATGAICCAGCGGGCCGCACAGCGCTGTGCGGIAATGGATAA 88
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2.3%; Score 33.8; DB 9; Length 3369400;
64.3%; Pred. No. 3.3c+02;
ive 0; Mismatches 27; Indels 6; 0
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08-03-963-965-2052
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Host Local Similarity 48.9%; Pred. No. 1.3;
Matches 90: Conservative 0; Mismatches 94:
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ne : 286 secs
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                                                                                                                                                                                                      871 TGAGATTTGCGGGACCG 887
     2.3°
Post Local Similarity 64.9°
Matches 50; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AW380639 RCZ-HT027 BM615374 :70506871 AV551507 AV551507 BM582957 170006872 AL064465 Drosophil AV629284 AV629284
SUMMARIES	ID	AW380638 BM615374 AV551507 BM582997 CNS0037Q AV629284
	DB	100 100 100 100 100 100 100 100 100 100
	Query Gore Match Length DB ID	280 551 533 678 1101
ď	Query Match	444444 45585
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BH767373 BMBAC348F AG117547 Pan troq1 RE442656 MHE1101 D	2 BOMEL07T ze63b10.s	H75593 yu05f04.rl AA019639 ze62g01.s	AA001557 ze46d06.s BC834011 350349 MA	B57961 CIT-HSP-201	AU109318 AU109318	AU010392 HS_5101_B AO555566 HS 5020 A	A1743670 wq41e06.x	AI346857 qp53e12.x	BQ247372 TaE25047G	AI289776 qwi2a01.x	BG052847 RHIZ2_14_	AU482699 RPCI-11-2	AQ478968 RPCI-11-2	BF48454Z WHEZ3Z4_G	AA833827 od62c06.s	H08687 v193e12.rl	B69197 CIT-HSP-205	BM392441 50071-2-1	BM393654 50072-2-1	AL077401 Drosophil	BM136789 WHE2617_E	2	~*	(Z)	a)	R63461 yi08a12.s1	\sim	BF252018 ESI419280	30	21	74
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ALIGNMENTS

AM380638 RCZ-HI0275-01:199-011-f11 HT0275 Homo sapiens CDNA, mRNA sequence. AW380638 AW380638.1 GI:6885297 EST. Furman.	Eukaryoča: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 280) HCG http://www.udwig.org.br/ORESIES. The FAPESP/LICR Human Cancer Genome Project Unpublished (1999) Coctact: Simpson A.J.G. Laboratory of Cancer Genetics Lidwig Institute for Cancer Research Rua Prof. Antonic Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil	Tel: +55-11-2704922 Fax: +55-11-2707001 Fax: +55-11-2707001 Final: asimpson@ludwig.org.br Fils sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?ti-RC2&t2=RC2-HT0275- 011199-011-111&t3-1999-11-016.44-1) Seq primer: puc 18 forward High quality sequence start: 37
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Asamizu, E., Nakamira, Y., Sato, S. and Tabata, S. A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
203630393
                                                                                                                                                                                                                                                                                                                                                                    ESI 06-SEP-2000
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizulekazusa.or.jp, URL:http://www.kazusa.or.jp/cn/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II: Brassicales; Brassicaceae; Arabidopsis.
(bases 1 to 533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 GCACAGCGCTGTGCGGTAATGGATAAAGGCCTGGTTGTAGAAACGCTGACCCAACAA-CA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 GAACCCCGTCTITCCGTTGATACCTGATCATCTTTTCTGTAACGAACCCAATTGCGGAT 346
                                                                                                                                                      533 bp mkNA linear EST 06-SEP-200
AV551507 Arabidopsis thallana roots Columbia Arabidopsis thallana
CDNA clone R2127f10R 5', mkNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GCTCTCTGATGATCTTTTAATGCGTCGTCATCTGGCTCTGTAACTAAACGCTATAAATTA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 CGTGGAGAATAACATATGAAATGGTTGGAAGAATCCATTATGGCCAAACGCGGTGTTGGT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                               10 TCCATGTGGCCGTGATCCTGGTCGAGCAGGATATTGCGATGATCCAGCGGGCCGCACAGC
                                                                                                                                                                                                                                           70 GCTGTGCGGTAATGGATAAAGGCCTGGTTSTAGAAACGCTGACCCAACAACAG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clonc="RZ127f10R"
/clone_lib="Arabidopsis thaliana roots Columbia"
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0
                                            Length 551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 6.5;
0; Mismatches 108; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 GCCGGGCGTAAACCGGTAACGCATCACCTGACGGAAGAAT 282
                                               DB 13;
                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organisme"Arabidopsis thaliana"
                                          Score 37.8; DB Pred. No. 2; 0; Mismatches
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/db_xref="taxon:3702"
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                                          2.6%;
ilarity 58.4%;
Conservative (
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Cuery Match
Best Local Similarity 50.77
Matches 112; Conservative
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                                          Query Match
Best Local Similarity
Matches 66; Conserv
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KEYWORDS
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                                 1. .280
/organism="Homo sapiens"
/do_ref="Less"
/do_ref="Less"
/do_ref="Less"
/dov_stage="Adult"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: pucl8; Site_1: Smal:
Site_2: Smal: A min1-library was made by cloning products
derived iron ORESIES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the PUC 18 vector. Reverse ::anscription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM615374 551 bp mRNA linear EST 25 FBH-2002 17000687146710 A.Cam.ad.cDNA.blood! Anopheles gambiae cDNA close 19600449698260 57, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   507 AATCCATGTTGCCCCGCGCGGTTGATCCCTACGGCATCTGCGCCATGATTCCGCATTIIG 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 551)
Holt.R.A., Lin.d.-J., Murphy,S.D., Evans.C.A., Kraft,C.i., Charlab.R., Collins,F.H., Venter.J.C. and Hoffman,S.L.
celera Anopholes gambiae EST project
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Neoptora; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                                    Length 280;
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                                                                                                                                                                                                                                                                                                                                                                  Score 39.6; DB 10;
Pred. No. 0.33;
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/clone="19f0f445698200"
/clone_llb="A.dam.ad.cDNA.blood1"
/dev_stage="Adult"
/lab_bos:-"DH10b"
                                                                                                                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        567 GCGGACTGACCGGGACCGACCTGACGGCCATGCT 600
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Tel: 2404533151
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High quality sequence stop: 1:1.
                      Location/Qualifiers
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Plate: NU01004AAO row: N
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Contact: Holt R.A.
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Chlamydomonas reinhardtii
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1 (bases 1 to 1101)
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                                                       MAS82997 678 22-FES-2002
17000667277353 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
19600449689205 57, mRNA sequence.
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                                                                                                                                                                                                                                                                            Holt. R.A., Lin. 3.79. Murphy, S.D., Evans, C.A., Kraft, C.L., Charlat, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Gerera Anopheles gambiae EST project
Unpulshed (2002)
Contact: Holt R.A.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila
                                                                                                                                                                                                       Eukaryota, Metazoa, Arthropoda, Hexapoda, insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocora, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="RSP-ST (Reduced suso, to Permethrin - std.
chromosome)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5%; Score 36.2; 89.13; Length 678; 57.5%; Pred. No. 7.7; utive 0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_119602449689205"
/clone_11b="A.Gam.ad.cDNA.bloc21"
/dev_stage="Adult"
/lab_host."D#10b"
                                                                                                                                                                                                                                                                                                                                                                                                45 w. Gude Dr., Rockville, MD 20852, USA
Tel: 2404533151
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 2404534580
Email: HoltzRAccelera.com
Plate: NU011084AC row: G column:
Seq primer: M13 Reverse.
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                                                                                                                                                                   African malaria mosquito.
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Best Local Similarity 57.59
Matches 65, Conservative
                                                                                                                                                                                         Anopheles gambiae
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                                                         BM582997
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DEFINITION
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ORGANISM
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AUTHORS
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KEYWORDS
               RESULT 4
BM582997
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Petermination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Drosophina Genome Project (BDGP).

Determination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Drosophina Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophina melanogaster genome using these BACs. For further information picase sec http://www.fruitfly.org The BDGP Drosophina melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV629284 AV529284 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii 5% to mRNA sequence.
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Genoscope.
Lirott Submission
Lirott Submission
Lirott Cabmission
Lirott Cabmission
Lirotted (02.5UN-1999) Genoscope - Centre National de Sequencage :
BP 191 9:005 EVRY cedex - FRANCE (F-mail : segrefegenoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 TIGGCCCIIATTCCACACCCGTCCTGACCATCGAACCCGGTGACCGGAITATTGICGACA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 AAATGCCCTTTCTCAACCCACAAAACGGACCGATCATGGTCAATGCCGCGGGGAAAGGTG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             753 ATKDKWGMKHKKKKKMKKKMDMKMDGAKATAWAMTRAGAVGAKARRAMKATRWAGARRVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81: KEGAMRVMKADAMRRMRHWARWANGAGHITVNMVBVNMGNGMKSKGMGNTKNKVNSVKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 GAGAATAACATATGAAATGGTTGGAAGAATCCATTATGGCCAAACGCGGTGTTGGTGCCG
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/db_xref="taxon:727"
/clone="aktroBk14"
/clone=1b=*RPC1-98"
/notc-*end: TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17;
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Local Similarity 12.2%; Pred. No. 11;
Les 49; Conservative 173; Mismatches 191;
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/db.xref_flaxon:6279"
/clone_lib="Brugia malayi Gencmic Bac Library 3"
/sex="Mixed (male and female)"
/tissuc_type="whole parasite"
/tissuc_type="whole parasite"
/dev_stage="microfilaria (L1)"
/dev_stage="microfilaria (L1)"
/rote="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
/rote="Vector: pBACe3.6; Site_1: BamH I; Brugia
/rote="Vector: pBACe3.6; Site_1: BamH I; B
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Pan troglodytes DNA, clone: PTB-125G18.F, genomic survey sequence.
AG117547
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Pan troglodytes
                                                                                                                                                                                                                                                                                      Email: mark.blaxter@ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire
Nahitron and Dr Mike Quail. The Sequence was generated by The
Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 TGTGCGGTAATGGATAAAGGCCTGGTTGTAGAAACGCTGACCCAACAACAGCTCTCTGAT 131
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
    Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
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Pujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AXG-2001) Asac Pujlyama, The Institute of Physical
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BAC end sequences of Library PTB
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54.2%; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edinburgh, UK.
Seq primer: SP6 (ATTIAGGTGACACTATAG)
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/strain="TRS"
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1. .482
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                                                                                                                                                                                                            Tel: +44 131 650 6760
Fax: +44 131 670 5450
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Best Local Similarity 54.2
Matches 71; Conservative
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/Glone="LCU055h05_".
/Clone=lib="Chlamydomonas reinhardti! 5% to 0.04% CC2"
//Clone=lib="Chlamydomonas reinhardti! 5% to 0.04% CC2"
//Ante="Vector: pBluescriptII SK+: Size_1: Eco2:: Size_2:
//Ante="Vector: pBluescriptII SK+: Size_1: Eco2:: Size_2:
//Ante="Vector: pBluescriptII SK+: Size_1: Bco2:: Size_2:
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                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-2812, Japan
Email: asamizuskazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Oualifiers
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                                                                                                                                                                 Ohyama, K.,
                                  Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                    Asamizu, E., Miura, K., Kucho, K., Incue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S. Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardti:

20539644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 CCACACCCGTCCTGACCATCGAACCCGGTGACCGGATTATTGTCGACACTGGAGATACTT
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Pred. No. 7.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3055"
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(bases 1 to 482)
Whitton, C., Daub, J., Wa
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Best Local Similarity 45.9%;
Matches 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE442656 611 bp mRNA linear EST 25-JUL-2000 WHE1101_D03_G052S Wheat etiolated scedling root normalized cDNA library friticum acstivum cDNA clone WHE1101_D03_G05, TRNA
and Chemical Research (KIKEN), Genomic Sclences Center (SSC), 1-7-22 Suchtro-chour, Isrurumi ku, Yokohama, Kanagawa 236-5045, Japan 1-7-22 Suchtro-chourumit, Ku, Yokohama, Kanagawa 236-5045, Japan 1-8-11 (E-mail.chimpbes4sc.fiken.go.jp, URL.http://kgp.gsc.riken.go.jp/.fei.81-45-503-9111, Fax:81-45-503-9170, Clones are derived from the chimpanace HAC library PTB This BAC end was generated during the R&D process and may have higher chance of olone tracking errors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1315 TACTCCTTCAGCGGAGTGACGGCGGCACAAGAGTTGTCACAATGGCGCGGGAGCAACCCAG 1374
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Peales, Poaceae, Peciden
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1 (bases 1 to 61)

Anderson, O.D., Chao, C., Choi, D.W., Close, T.J., Fenton, R.D., Han P.S., Hista, C.C., Kang, Y., Eazo, G.R., Miller, R., Mquycu, H.I., Rausch, C.J., Seaton, C.L., Tong, J.C. and Ihang, E.

The structure and function of the expressed portion of the wheat.
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186 c 160 g 198 t 3 cthers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-125G18.F"
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/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="lymphoblast"
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Sacī
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Contact: Olin Anderson
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sufface-sterlized, germinated and grown aseptically in
the dark at room temperature or filter paper with water,
nystatin and cefolaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA wore prepared, a cinA library was made in the
TJ Close lah (Choi, Close, Fencon) at the University of
California, Riverside. The cDNA clones were in vivo
cxtised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HI Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protectol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (al) other authors)."
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           719 GAAATTGACTCAATCACTGACGCCAGACAATCACGGCGGGAATATGGATGTGCCG 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20] AATCTAAGCAGAGGTTCCAAAGTTTATCTACAGTTGAAGGAGCAAATCTGAGT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; curosids II: Brassicales; Brassicaceae; Brassica.
                            /close_!ib-"Wheat ctiolated seedling root normalized cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                779 GATATAGGACCAGGGAGTATTACCTATCTGCCGGTACGTGCGCCTGGAGGCCGCCTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cdtownétigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGGTGATGCCCATGCTTGTCAGGGTGATGGTGAGTTT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26: ACTGGCGATATGCACITTTCCCAAGGTGATGGTGAAGTCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
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/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4%; Score 35.2; D 51.2%; Pred. No. 15; tive 0; Mismatches
/clone-"WHE1101_D03_G05"
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                                                                                                /tissuc_type-"Root"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica oleracea.
Brassica oleracea
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: TF
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/clone_lib-"Soares fetal liver spleen lNFLS"
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MEDLINE
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H75593/c
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Nammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (Dases: 1.0.268)

2 (Dases: 1.0.268)

2 (Dases: 1.0.268)

3 (Dases: 1.0.268)

4 (Dases: 1.0.268)

5 (Dases: 1.0.268)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 bp mRNA linear EST 36-JAN-1997 ze63bl0.s1 Soares retina N204HR Homo sapiens cDNA clone
IMAGE:363643 3' similar to WP:KO2A2.3 CEC2791 BURETANIDE-SENSITIVE
NA-K-C1 COTRANSPORTER ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissuc_type="retina"
/dev_stage="55 year oid"
/dev_stage="55 year oid"
/lab_most="print"
/lab_most="print"
/lab_most="Organ: eye content print"
modified polylinker; Site_1: not I; Site_2: Eco RI; lst
strand cDNA was primed with a Not I; - oliqo(dT) primer [5]
                                                                                                                                                                                                                                                                                                                                              636 GGACTTCCTCGAIAAGACGGCGTCATATCAAGCAGAGTTCTTTCTAAGAAATCGTAAAAA 577
                                                                                                                                                                                                                                                                                                                                                                                            652 GGTCTACTSGAGCAAACGCCATACGCTTCCCTATAAACCCCATATTGGCACCTTGAGGGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.lls1.gov) for further information.
Insert Length: 2350 Std Error: 0.00
Seq primer: -40413 fwd. from Amersham
High quality sequence stop: 171.
Location/Qualifiers
                                                                                                                                                                                                                                                                                               592 GGCCATGCTCAATGATCCGCTGCCAGAAAAGGTGCGCATGATTAAACTCGACAGTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                        576 CGTCTAAGTCGAAAAACGGCCAAAAAGAGGCCTAGAACGGGGGCTAACAGGCCAGTTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               712 ATCGCCAGAAATTGACTCAATTCACTGACGCCAGACAATGACGGGGAATA 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        516 TECATACGAAATTGAGGCCATCAGTGCTATGACGGTTTATCTTTACTTGGGGAAAA 461
                                                                                                                                                                                                                                                   Gaps
                    /clone="BCMEL07"
/cione_lib-"BO_2_3_KB"
/note="Vector: pH0S1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inscribed into pH0S1 using BstXI linkers"
i 165 c 181 g 251 t
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                             DB 17; Length 772;
                                                                                                                                                                                                                                              88; Indeis
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/organism"Homo sapiens"
/db_xref="CDB:1280346"
/db_xref="taxon:9606"
/clone="IMAGE:365643"
/clone_lib="Soares retina N2b4:RR"
                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                             2.4%; Score 35.2; 1
0.0%; Pred. No. 18;
/db_xref-"taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA020733.1 GI:1484516
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                                                                                                                                                                                                                      50.0%;
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                                                                                                                                                                                                                                           88; Conservative
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Best Local
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DEFINITION
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JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                Matches
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KEYWORDS
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Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Manamalia; Eutheriu; Primates; Catarrhini; Hominidae; Homo.

(Dassa: 1 to 421)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoes, J., Dietrich, N., Diduque, T., Favelio, A., Gish, W., Hawkins, M., Mortis, M., Rucaba, T., Lacy, M., Le, N., Mardis, E., Moore, R., Mortis, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schelienberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohlfing, T., Waterston, R., Wilson, R. and Marra, M. Generatico and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 bp mRNA linear EST 01-NOV-1995 yu05f04.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:232927 5', mRNA sequence.
535 CTACGGCATCIGCGCCATGATICCGCATTTTGGCGGACTGACCGGGACCTGACGGC 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 CAAGGACTICTTCAGCATGAAGCGGGAGTGGGAGAACTTGAACCAGTGCAACGTGCGGCG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    595 CATGCTCAATGA7CCGCTGCCAGAAAAGGTGCGCATGATTAAACTCGACAGTGAAAAGGT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 CATGCACACTGNCGTGGGGTGAACGAGGTCATCGTGAAGAAATCCCGGGACGCCAAGCT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wsstl.edu
Insert Size: 1012
High quality sequence stops: 366
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL: contact the :MAGE Consortium (info@image.llnl.gov) for further information.
seq primer: MIRPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University Schoo! of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63:08
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                         2.4%; Score 35; DB 9; Length 268; 50.6%; Pred. No. 9.8; ive 0; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         655 CIACTGGAGGAAACGCCATAGGCTTGCCTATAAAGCCCGTATATTG 698
                                                                                                                                                                                                                                                                                                       4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 TGTTTTGCTGAACAIGCCIGGGCCTCCCGGCAACGGAAIGGTG 4
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/db_xref="GDB:3786104"
/db_xref="taxon:9606"
/clone="IMAGE:232927"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 50.6
Matches 83; Conservative
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Mor, Jul

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human.
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DOCUS
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ORIGIN
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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                                            Vince Torgan: Liver and Spieon: Verbor: pT7TFO (Phothacia) with a modified polylinker: Size_1: Fac I; Size_2: Ecc RI; stranded CDNA was princed with a Pac f - oligo(dl) primor is AACTGGANGAATTAAATTAAAATCTITTITTITTITTIT : 3', double-stranded CDNA was ingated to Ecc RI adaptors (Pharmacia), digested with Pac I and cloned into the Fac I and Ecc RI sizes of the modified pT7T3 wenter. Library went through one round of normalization, Library went through one round of normalization, Library in 10 constructed by 3 ento Scares and M.Patima Bonaldo.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens

Eukaryota: Marazoa: Clordata: Craniala; Vertebrata: Entelecatom::

Maramalia: Eutheria: Plimates; Catarrhini: Hominides; Homo.

(bases: to 41)

Hilleri. Lennon.G. Becker,M. Bonaldo,M.F., Chiapelli.F.,
Chissoe,S., Dierrich,N., Dubque,T., Favello.A., Gish,W. Hawkins,M., W. Hultman,M., Rucdab.T., Lacy,M., Le,N., Le,N., Mardis,E., Schellenberg,K., Scares,M.B., Tan.F., Thierry-Meg.J., Trevaskis,E., Schellenberg,K., Scares,M.B., Tan.F., Thierry-Meg.J., Trevaskis,E., Uncertavook,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 numan expressed sequence lags.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1044 ACTGGCTGGTAGAAGACTTTGGCTTCGAACAATGGGATGCCTACATGCTTCTGAGTCAAT 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1104 GCGGCAAAGTGCGGCTGGGCAACATGGTCGACCCCAAATACACGCGTTGGCGCGATGCTGA 1163
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Ze62g01.sl Soares retina N2b4HR Homo sapiens CDNA clode
IMAGE.36360C 3' Similar to WP:KC2A2.3 CE0279: HUMETANIDE-SENSTTIVE
NAK C.I COFRANSPORTER:, RRNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ACTGGGAAGAAGATGACTTTGGCCTGCGAGGAGATGATCTCAACGCAGGTCTGAGACAAT 183
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This cione is available royalty-free through LLNE ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2016 Std Error: 0.00
Seg primer: -40M13 fwd. from Amersham
High quality sequence stop: 360.
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                                                                                                                                                                                                                                                                                                                                                        2.4%; Score 35; DB 14; Length 421; 51.6%; Pred. No. 13; cive 0; Mismatches 75; Indeis
/dev_stage="20 week-post conception ferus"
/lab_host-"FH10B (ampicillim resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 ACTATACTITATAA;AGAGCTGATCTITCTACCC 88
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Eukaryota Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 492)
Hillier,L., Caarx,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffith,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldman,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGC1557
492 bp mRNA linear EST 29-NOV-1996
246406.51 Scares retina N254ER Homo sapinas CDNA clone
120Ac2-35,027 3' similar to WP-KCDA2.3 CED2791 BUMETANIDE-SENSITIVE
NA-K-C1 COTRANSFORTER ; contains Alu repetitive element; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          535 CTACGGCATCIGCGCCAIGATTCCGCATTITTGGCGGACCGGGACCGACCTGACGGC 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 CAAGGACTICITCAGCATGAAGCCGGAGTGGGAGAACTIGAACCAGTCCAACGTGCGGCG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108
1419 134 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 est@warson.wustl.edu
This clone is available royalty-free through LLNi; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 3433
Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                         of Toronto, Library constructed by Bento
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Best Local Similarity 50.5%; Pred. No. 14;
Matches 83; Conservative 0; Mismatches 81; Indels
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/tissuc_type="retina"
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/lab_host="DilUB (ampicillin resistant)"
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Scg primer: mob.REGA+ET
High quality sequence stop: 233.
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Contact: Wilson RK
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                                                        Single pass sequencing, Bases called and alltrimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore land -minmatch 12 options.
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1 (bases 1 to 505)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595 CATGCTCAATGATCCGCTGCCAGAAAGGTGCGCATGATTAAACTCGACAGTGAAAAGGT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 CATGCACACTGACGGGGTGAACGAGGTCATCGTGAAGAAATCCCGGGACGCAAGCT 48
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EST discovery in swine
Unpublished (2000)
Contact: Smith TPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 CTACGGCATCTGCGCCATCATTCCGCATTTTGGCGGACTGACCGGGACCTGACGGC
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BG834211
RG834211.1 GI:14199291
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PO Box 166, Clay Center, NE 68933-0166, USA
                              /clone_lib="Soares retina N2b4HR"/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 III P. N.A.
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Seq primer: ATTTAGGTGACACTATAG.
'db_xref="taxon:9606"
               /clone="IMAGE:362027"
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Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                      2 CCGGGAACTCCATGTGGCCGTGATCCTGGTCGAGCAGGATATTGCGATGATCCAGCGGC
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us-10-086-082-2.rag

Page 1

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compagen Ltd.
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protein - protein search, using sw model Š July 3, 2003, 15:36:56 : Search time Pr Seconds (without alignments) 533.002 Million cell updates/ser Run on:

US-10-086-082-2 1746 1 MKWILESIMAKRGVGAGKKP.....GNCVCPRVIVGAMLKKNLLV 328 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 Total number of hits satisfying chosen parameters:

908470 seqs, 133250620 residues

Searched:

length: 0 length: 2003000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/SIDS2/qcgdata/genescq/qenescqp-emb//AA1999.DAI:*/SIDS2/qcgdata/genescq/qenescqp-emb1/AA2006.DAT:*/SIDS2/qcgdata/qenescq/qenescqp-emb1/AA2031.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
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Result.	Score	Query Match	Query Match Length DB	DB	ID	Description	
1	1731	0.65		19	AAW40253	K. OXVEGGA RESPECT	
7	355.5	20.3	3.5	21	AAB29631	Entercharter close	
e	233	13.3		23	ABB47924	Listeria monocytos	
4	208	11.9	•	23	ABB93276	Herbicidally activ	
S	198	11.3	452	21	AAG09237	Arabidopsis thalla	
9	198	11.3	Ī	21	AAG50180	Arabidopsis thaila	
7	178	10.2	·	21	AAG09208	Arabidopsis thalia	
8	178	10.2	Ī	21	AAG50181	Arabidopsis thalia	
6	177.5	10.2	-	19	AAW58856	C. acidivorans dam	
10	174.5	10.0	-	21	AAG09209	Arabidopsis thalia	

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ALIGNMENTS

AAW40263 standard; Protein; 328 AA. AAW4 0263

(first entry) 7 16-JUN-1998 AAW402637

K. oxytoga R-specific amidchydrolase protein. ŽŽ

R-specific anidohydrolase: hydrolysis; racemate; nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform. Klebsiella oxytoca W09801568-A2

15-JAN-1998

97WO-EP03670. 97CH-0000500. 96CH-0001723. 03-MAR-1997; 10-JUL-1996; 10-001 1997;

(LCNZ) LONZA AG.

Tinschert A; Shaw N, Naughton A, Robins K, Brieden W, Na Zimmermann T;

WPI; 1998-101063/09. N-PSDB; AAV10449

Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation

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                                                                                                                                                                                                                            This sequence represents a R-specific amidohydrolase isolated from Klebsiella oxytoca strain PRS1 which allows the microorganism to utilise 3,3,3-trifluoro-2-hydroxy-2-methy, propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using
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                                                microorganism or derived enzyme, used as drug intermediate
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                                                                                                                                      Page 34-35;
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                                                                                                                                                               The invention relates to a novel amidase, and the gene encoding the novel amidase, from interobacter cloacae. The novel amidase stereoselectively hydrolyses alpha-amino acid amides and alpha-hydroxy acid amides to give optically active alpha-amino acids and alpha-hydroxy acids. The invention also relates to variants of the novel amidase which retain activity, recombinant vectors and host cells containing the novel amidase gene, and recombinant production of the novel amidase gene have remarkably elevated catalytic capability as compared to those produced by conventional methods. The present sequence represents the novel Enterobacter cloacae amidase.
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                                 Novel amidase gene encoding protei: which stereoselectively hydrolyzes alpha-amino-acid amides and alpha-hydroxy-acid amides, with enhanced catalytic capability to yield optically active alpha-amino-acids and
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vitamin B12; bacterial infection; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                      20.3%; Score 355.5; DB 21; Lenyun
31.9%; Pred. No. 6.5e-28;
Mismatches 136; Indels
                                                                                                                               Claim 1; Page 20-22; 32pp; Japanese
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N-PSDB; AAC64148, AAC64149.
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es 190; Conservat
                                                                                             alpha-hydroxy-acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the genome sequence of distorial monocytogenes EGP-e (see ABA03041). The genome sequence and fragments of the are useful for selecting probes and primers for detecting genes is L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and its biosynthesis and biodegradation, especially biosynthesis of vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.

Specification, but was obtained in electronic format directly from WIPO at the printed and the contraction of an electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 IYIBERARRODLLAITIEKIRLLGTEVFELNG--PN:-GITDBLLIS------NSTROYK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 VENNQIIYSEDIHIPIRKTIGLL - - - KTEELNPSKVPTKNGGLLCSSKITEGATIFLPV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>~</u>.
                                                                                                                                Cossar: P;
                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence for Listerly monocytogenes, useful e.g. for treatment and prevention of Listerla and related bacterial infections, and related polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMVNGAEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGLIGTDLIAMINDPLPHKVEMIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDSEKVYWSKRHILPYKPHIGTLSVSPEIDSIN-SLTPNNHGGNMDVP91GPGSITTTPLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMEKS------TEPALRVKDGSVVKIKTKDHENGGIHAKGLHYGELDWKOF-SPITTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAPGGRLF1GDAHACQGDGE1GGTAVEFAS1TTIKVDLIKNWOLSWPRMENAENINSIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 EKYGASLHVGNVRATTGFCKITATSAEAPAEVTLRLQILKNRTAPTPTLIHYENLICLAS
                                                                                                                                                                            Amend A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 ARPLEDATRIAYRDLIYWLVEDFGFEQWDAYMLLSQCGKVRLGNMVDPKYTVGAML 322
                                                                                                   Fsih: H, Dehoux P:
                                                                                                                                                                                                      Durant L:
                                                                           Buchrioser C, Frangeul S, Couve E, Russian C, Lunt F, Cossant Dussurget O, Chotowani F, Nedjari H, Glaser P, Kunst F, Cossant Daniels J, Goebel W, Freft J, Kuhn M, Ng E, Vazquez-Boland JA. Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend J Charraborty T, Domann E, Hain T, Berche P, Charbit A, Dusant L: Perez-Diaz J, Baquero F, Garcia Dei Portillo F, Gomez-Lopez N: Lin Da Pablos B, Wehland J, Kaorst U, Entlan K, Hauf J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID No 629; 192pp: French.
11-APR-2000; 2000FR-0004629
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                                                 (INSP ) INST PASTEUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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ABB93276 standard; Protein; 432 AA

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85 NGPIMV----NGAEKGDVLAVYIESMEPRGVDPYGICAMIPHFGGEIGTDLTAMENDPI, 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 QODQPLHNRWHPEIPPVAEVKAGEFFRVEMIDAMGGVIKDNDSASDIKN--LVLITIHHL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P---- - CATKAIMYFEGIYAYSPQIPGVRFPGLTHPGVIGTAPSNELLRIWNDRERQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMQKEPHYTTGPYSTPVL.TTEPGDRIIVDTRDAFEGAI---NSEQDIPSQLLKMPFLNPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 LEESGVESLTICEIEEGTPEWERLANEARTIPGRENGGNCDIKNISRGSKIYLPVFVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRLFIGDAHACOGDGEL--CGTAVEFASITTIKVDLIKNWQLSW-----PRMENAENIMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; SEQ ID NO 2487; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 PEXVEMIKIDSEKVYWSKRHTLPYKP------HIGTLSVSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Score 208; DB 23;
; Fred. No. 1.8e-12;
44; Mismatches 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQCG-KVRLGNMVDPKYTVGAM 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 - EIDSINSL-----TPD---
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24.1%;
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Matches 92;
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                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                             Arabidopsis thallana protein fragment SEQ ID NO: 7049.
                                                             AAG09207 standard; Protein; 452 AA.
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                                          Arabidopsis thaliana protein fragment SEQ ID NO: 63561.
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hybridisation assay: genetic mapping; gene expression control; promoter:
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                                                                                                                                                                                                                                                                                                                                                                         | UDPYGI -----HFGGLT--GTDLIA 133
                                                                                                                                                                                                                                                                                                                                                                                                  61 GDEWGFTGSFDRENGGGFLTDHFPCATKAIWYFEGIYAYSPQIPGVRFPGLTHPGVIGTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 MINDPLPEKVRMIKLDSEKVYWSKRH------ILPYKPHIGTLSVSPE----ID 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ----PSNELLRI------WNDRERQLEESGVESLILCEVVHORPLACLPTTKGCLLG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 SINSLIPD--------NHGGNMDVPDIGPGSITYPLVRAPGGRLFIGDAHACQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DAMGGVIKDNDSASDIKN--LVLTTHHLSGPIRVVDEEGVAAKAGDLLAVEICNLGPLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 ODGET--CGTAVEFASITTIKVDLIKNMQLSW----PRMENAENIMSIGSARP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guery Match 10.2%; Score 178; DB 21; Length 404;
Best Local Similarity 25.4%; Pred. No. 2e-09;
Matches 94; Conservative 40; Mismatches 112; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 63562.
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990S-0160767.
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990S-0160815.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 VDPKYTVGAM 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 VDSPSAVATL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thallana
                                                                                                                                                                26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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Gaumma-lactamase; enantiomer; bicyclic lactam; temperature stable;
2-azabicyclo(2.2.1)hept-5-en-3-one; therapeutic agent; antiviral;
cardiac vasodilator.
                                                                                                                                                                                                                                                              Lactamase enzyme specifically hydrolysing (+)-enantiomer of 2-
azaiblicyclo(2.2.1)hept-5-en-i-one - isolated from Comamonas
acidivorans or prepared by recombinant DNA technology, used as,
cardiac vasodilator

    C. acidivorans gamma-lactamase pretein.

                                                                                                                                                                                                                                                                                                              Claim 5; Page 17-20; 28pp; English.
                      23-JUL-1998 (first entry)
                                                                                                 Comamonas acidivorans
                                                                                                                                                                                                                                    WPI: 1998-193625/17.
                                                                                                                                                                                                                  Brown RC, Lee CS,
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                                                                                                                                                                                                                                                                                                                                                                                                                              61 GDEWGFTGSFDRENGGGFLTDHFFPGATKALWYFFGLYAYSDQTPGVRFPGLTHPGVIGTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEGISVDESGKOHYLDAI-VAYKRAVLNAIDYLFKFGYSKEQVYLLLSCCPC5GRLSG: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 MENUPELPEKVRMIKEDSEKVYWSKRH-----TEPYKPHIGTESVSPE----ID 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PSNELLRI-------WNDRERQLEESGVESLTLCEVVHQRPLACLPTTKGCLLG 167
                                                                                                                                                                                                                                                                                                                                                                                                           DAMGGVIKDNDSASDIKN--LVLTTHHLSGPIRVVDEEGVAAKAGDULAVETONIGPUP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SINSLIPD-------NHGGNMDVPDIGPGSITYPLVRAPGGRLFIGDAHACO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 NIEEGTPEWERIANEAARTIPGRENGGNCDIKNLSRGSKIYLPVFVEGANLSTGDMEFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIXGET -- CGTAVEFASITT: KVDLIKNWQLSW-----PRMENAENIMSIGSARP-----
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                                                                                                                                                                                                                                                                                                                                                                       Indels 124;
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99US-0160770.
99US-0160814.
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990s-0160989.
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                                                                                                                                                                                                                                                                                                                                                             Similarity
29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
08-OCT-1999;
12-OCT-1999;
13-OCT-1999;
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26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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22-0CT-1
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14-0CT-1
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------YIESMLPRGV----D 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 PYGICAMIPH-----FGGLTGTDLTAMI,NDPLPEKVRMIKLDSFKVYWSKRHTLPYKPHI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTLSVSPE------GTLSDAGGNMDVPDIGPG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 PYSTP------VLIIEPGDRIIVDTRDAFEGAI---NSEQDIPS-QLLKMPFLN 82
This sequence represents a gamma-lactamase capable of hydrolysing an enantioner of the bicyclic lactam 2-azabicyclo(2.2.1)hept-5-en-3-one. This enarghe has at least 1 of the following features; greater than 8% retention of activity after incubating at 40 deg. C for 4 hours, or >30% activity after incubating at 60 deg. C for 4 hours, hydrolysis at an initial concentration of 10° g racemic lactam plus 30° ml buffer and proceeding to a least 90 (especially at least 90% hydrolysis of the (+) lactam with 65% hydrolysis of the (+) lactam with 65% hydrolysis of the (-) lactam. The enzyme is much more temperature-stable than previously identified (-)-gamma-lactamases used for the same purpose. It also enables the bloresolution to be exercised out at very high substrate/product concentrations. This enzyme has applications as a therapeutic agent e.g. as an antiviral agent or as a cardiac vasodilator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 PYDNPQVHNRWHPDIPMAVWVEPGAEFKLETYDWTGGAIKNDDSAEDVRDVDLSTVHFL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 FHGMFTKSRHIPGVNFAGLIHPGLIGCLPDP-----KML-----ASWNERET-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 575;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%; Score 177.5; DB 19; 24.0%; Pred. No. 3.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 PQNGPIMVNGAEKGDVLAV------
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263 SRVFFPVYVDGAGLSVGDLHFSQGDGEITFWGP1EMPGWVHMKVSLIK 310

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AAW58856 standard; Protein; 575 AA

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08-301-1999;
09-301-1999;
12-301-1999;
13-301-1999;
14-301-1999;
16-301-1999;
16-301-1999;
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16-AUG-1999;
17-AUG-1999;
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                                                                                                                                                                                                                             Protein identification; signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ 1D NO: 7051
                                                                       AAG09209 standard; Protein; 400 AA.
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99US-0139456.
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                                                                                                                                                  17-0CT-2006 (first entry)
                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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07 - JUN - 1999;

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10 - JUN - 1999;

14 - JUN - 1999;

16 - JUN - 1999;

16 - JUN - 1999;
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10-APR-1999

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21-APR-1999

23-APR-1999

28-APR-1999

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05-MAR-1999;
09-MAR-1999;
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990S-0144352 990S-0144352 990S-0144814 990S-0144814 990S-0145088 990S-0145088 990S-0145089 990S-0145089 990S-0145089 990S-0145089 990S-0145089 990S-0145918 990S-0145918 990S-0145918 990S - 0146388 990S - 0146389 990S - 0147038 990S - 0147302 990S - 0147302 990S - 0147303 990S - 0147416 990S-0139457. 990S-0139458. 990S-0139465. 990S-0139461. 990S-0139462. 990S-0139462. 990S-0139462. 990S-0139463. 990S-0147935. 990S-0148171. 990S-0148319. 990S-0148341. 990S-0148684. 990S-0148788. 9905-0140353 9905-0140923 9905-0140921 9905-0140991 9905-014091 9905-014235 9905-014235 9905-014235 9905-014235 9905-014235 9905-014235 9905-014235 9905-014235 9905-014235 9905-014435 990S-0144332. 990S-0144333. 990S-0144334. 990S-0144335. 18 - JUN - 1999 23 - CJU - 1999 24 - CJU - 1999 25 - CJU - 1999 26 - CJU - 1999 27 - CJU - 1999 28 - CJU - 1999 29 - CJU - 1999 20 - CJU - 1999 21 - JUN - 1999 22 - CJU - 1999 23 - CJU - 1999 24 - CJU - 1999 25 - CJU - 1999 26 - CJU - 1999 27 - CJU - 1999 28 - CJU - 1999 29 - CJU - 1999 20 - CJU - 1999 20 - CJU - 1999 20 - CJU - 1999 21 - CJU - 1999 22 - CJU - 1999 23 - CJU - 1999 24 - CJU - 1999 25 - CJU - 1999 26 - CJU - 1999 27 - CJU - 1999 28 - CJU - 1999 29 - CJU - 1999 29 - CJU - 1999 20 - C

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SVDESGRQHYLDAT-VAYKRAVLNAIDYLFKFGYSKEQVYLLLSCCPCEGRLSGIVDSPS 346
                                                                                                            -----LEDATRIAYRDLIYWLVE---DFGFEQWDAYMLLSQCG-KVRLGNMVDPKY 316
118 SNELLRI------WNDRERQLEESGVESLTLCEVVHQRPLACLPTIKGCLLGNIEEG 168
                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                              --CGTAVEFASITTIKVDLIKNWQLSW----PKMENAENIMSIGSARP-----
                     TPD-----NHGGNMDVPDIGPGSITYPLVRAPGGRLF1GDAHACQGDGE1
                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 63563.
                                                                                                                                                                                                                                   AAG50182 standard; Protein; 400 AA.
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99US-0123180.
99US-0123788.
99US-0125788.
99US-0126785.
99US-0127465.
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99US-0129845.
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                                                                                                                                                                              347 AVATL 351
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25-MAR-1999;
29-MAR-1999;
61-APR-1999;
06-APR-1999;
08-APR-1999;
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28-APR-1999;
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21-MAY-1999;
24-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121; Gaps
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        990S-0149723.
99US-0149929.
99US-0149902.
99US-0150566.
99US-0150884.
99US-0151065.
99US-0151065.
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28-0CT-1999;
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23-SEP-1999;
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K-1999; Y-1999; X-1999;	1999	1999	1999	1999	1999	1999	666T.	1999	5551	1999	1999	6665	555T.	1999	1999	9861	666T.	-1999	-1999	9661-	666T-	-1999	-1999	-1999	-1999	-1999 -1000	566T-	-1999	-1999	-1999	1999	- 1999	-1999	266T-	-1999	- 1999 - 1996	-1999	-1999	7661 -	-1999	566T-	2555T-	-1999	-1996	1999	-1990	-1999	-1999	-1999	-1996	- 1990	-1996
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03.AUG-1999;	- Aug 1999	1-AUG-1999	3-AUG-1999	3-AUG-1999	5-AUG-1999	5-AUG-1999	3-AIIC-1999	2-2116-1499	0-81G-1999	1-ATG-1999	566 - 504 - 7	3-AIIG-1999	3-AIR-1999	5-AIIG-1999	6561-001-2	00001-014-0	00000 0000 0	5557 - 53W - 5	665 - 108 - 1	J-AUG-1989	9 - AGG - 1999	3 - AGG - 1999	5-Aug-1999	6 - AUG - 1999	7-AUG-1999	7-AIIG-1999	7-AJG-1999	C-AGG-1999	1-AUG-1999	1-SEP-1999	7-SEP-1999	C-SEP-1999	3-SEP-1999	0001-045-9	6561-638-9	0-01-045-0	0 SEF 1333 0-SEF-1666	6661-336-8	0001 400	5501-433-e	0001 445-0	9-8E-13-8	4-0CI-1988	6661-130-6	6-04B 1999	9-7-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	0501 100-0	2-001-100-2 0001-100-2	0001-600-8	5561-EUU-8	5566-100- 8	0001 TOO 1	0001-100-4	666T - 100-4	0001-100-5	4 - 1 - 1 - 1 - 3	0001-100-1	0001-1333	666T-TOC.	6661-100-1	1-001-1999	1-00T-1999	1.OCT-1999	2-0CT-1999	2-0CT-1999	2-0CF-1999	5-0CT-1999	6561-100-5	0001 100 0	0001 1000	666.	6-0CI - 1668	$6 - 0 \le 1 - 1999$	8-0CI-1399	8-00T-1399
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ANW40264-W40275 are portide fraqments of an R-specific amidohydrolase solated from Klabsielia oxytoca strain PRS1. This enzyme allows the microarganism to utilise 3,3,3-trifluoro-2-hydroxy-2-methyi propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3,3,3-trilluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha
                                                                                                                                                                                                                                                                                   ABB93277 standard; Protein; 307
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                                                                                                                                                 8.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
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                                                                                                 -methylbenzylamine
                                                                                                                                                            Similarity
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Best Local Simi
Matches 62;
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                                                                                                                                                                                  139 LPEKVRMIKLDSEKVYWSKRH------TLPYKPHIGTLSVSPE----IDSLNSL 182
                                                                                                                                                                                                           118 SNELLRI ------WNDRERQLEESGVESLTLCEVVHQRPLACLPITKGCLLGNIEEG 168
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                                                                                                                                                                                                                                  -----NHGGNMDVPDIGPGSITYPLVRAPGGRLFIGDAHACQGUGEI
                                                                                                                                                                                                                                                                                --CGTAVEFASITTIKVDLIKNWQLSW----PRMENAENIMS1GSARP-----
                                                                                                                                                                                                                                                                                                       229 SFCG-ALEMSGFLELKCELIRNGMQEYLIPMGPIPLHVNPIFEIGPVEPRFSENLV: EGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation - by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R-specific amidohydrolass, hydrolysis, racemate, nitrogen sourse; 3,3,2-trifluoro-2-hydroxy-2-methy, propionamide, isoform.
                                       Length 400;
                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K. oxytoca R-specific amidohydrolase peptide T13-3.
                                       DR 21;
                                   10.0%; Score 174.5; CB 21; 24.7%; Prod. No. 4.5e-09; iive 41; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shaw N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10.2; Page 29; 68pp; Gcrman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robins K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 3 AA
                                               larity 24.78;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW40275 standard: Protein;
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 99US-0161993
              99US-0162142
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96CH-0001723
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                                               Local Similarity
tes 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                              317 TVGAM 321
                                                                                                                                                                                                                                                                                                                                                                                                       AVATL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LONZ ) LONZA AG.
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Zimmermann T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09801568-A2
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              29-OCT-1999;
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28-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identifying target proteins. (ABB$90790-ABB$4016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using statable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 TEEMQKEFHYTIGPYSTPVLTIEPGDRIIVDTRDAFEGA! -- - NSEQDIPSQLLKMPFLN
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; SEQ ID NO 2488; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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23.9%; Pred. No. 0.00012;
live 26; Mismatches 95;
Score 148; DB 19;
Pred. No. 5.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herbicidally active polypeptide SEQ ID NO 2488
                                                                                                                    110 GVDPYGICAMIPHFGGLTGTDLTAMI,NDPLPEK 142
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herbicidal; plant; agriculture; herbicide
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FEHYLIGPYSTPVLTIEPGDR
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                                                                                        ABB49158;
                                                                                                                                                                                                                                                                                                                                                                                                      Rose M,
                                                        AHB49158
                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW40264-W40275 are peptide fragments of an R-specific amidohydrolase isolated from Klebsiella oxytoca strain PRS1. This emixpro allows the microorganism to utilise 3.3.3-trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a propess for preparing (R) isologram of 3.3.3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychine or (S)-(-)-alpha
TOPLENREH ---- PEIPSVADVKTGELFRVENVGAVKENGSAGDIKS -- EDLSTVH 75
                                                  76 YESGPIKVVDEDGVAARPGDLLAVEICNLGPLPGDEWGFTASFDRENG-----GGFLTD
                              PONGPIMY-----NGAEKSDVLAVYIESMLPRGVDPYSTCAMIPHFGGLISTSLTAMIND
                                                                                                                    198 PGSTTYPLVRAPGGRLF1GDAHACQGDGB1--CGTAVEFASJTTIKVDLIKNWQLSW- -
                                                                         38 PLPEKVRMIKLDSEKVYWSKRHTLPYKPHIGTJSVSPELUSINSJAPONHGGNMDVPDJG
                                                                                                                                         -----GANLSTGDMHFSQGDGELSFCG-ALEMSGFLELKGELTRNOMQEYLTP
                                                                                                HEF-----CATKAIWYFEGIYAYSPOI-----PE------CATKAIWYFEGIYAYSPOI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triifluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate
                                                                                                                                                                                                                                                                                                                                 R-specific amidohydrolase, hydrolysis, racemate, nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methy, propiceamide, isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sength 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tinschert A:
                                                                                                                                                                                                                                                                                                              K. oxytoca R-specific amidohydrolase peptide T9-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.7%; Score 117; DB 19;
100.0%; Pred. No. 4.7e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shaw N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10.2; Page 29; 68pp: German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robins K,
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                                                                                                                                                                 253 -- PRMENAENIMSIGSARP 269
                                                                                                                                                                                      201 MCPITLHVNPIFEIGPVEP 219
                                                                                                                                                                                                                                            AAW40272 standard: Protein; 2)
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96CH-0001723.
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brieden W, Naughton A,
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Best Local Similarity
Thes 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-101063/09
                                                                                                                                                                                                                                                                                                                                                                   Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LCNZ ) LONZA AG.
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10-JUL-1996;
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The present invention relates to the genome sequence of Listeria monocytogenes EGD-c (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and related organisms. The present invention. Protein enroided by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for bicsynthesis and biodegradation, especially biosynthesis of vitamin E.2. The genome sequence are expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and woodcines on proteins encoded by it are useful in pharmaceutical and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and modulate L. monocytogenes-related diseases. In addition, the genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eal L. Couve E. Rushiok C. Fsihi H. Dehoux P. ani F. Nodjari H. Glaser P. Kurst F. Cossart P. Kurh L. Kuhn M. Ng E. Vazquez-Boland JA. Garrido-Garcia P. Tierrez-Martinez A. Amend A. nn E. Hain T. Berche P. Charbit A. Durant L. ro F. Garcia Del Portillo F. Gomez-Lopez N. vos B. Wehland J. Kaerst U. Entian K. Hauf J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment
and
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                                                                                                                                                                                                                                                                                                                                        Antibactorial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genemic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 238;
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22.2%; Pred. No. 0.019;
Live 24; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Couve E,
                                                                                                                                                                                                                                                           Listeria monocytogenes protein #1862
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    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchrieser C, Frangeal L, Cour
Dussurget O, Chetonani F, Nedi
Lanels J, Goebel W, Kreft J,
Domhoguez-Bernal G, Gartido-Gar
ABB49158 standard; Protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II-APR-2000; 2000FR-0004629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chakraborty T, Domann E,
Perez-Siaz J, Buquero E,
Maduenio E, De Pablos B,
                                                                                                                                                                      (first entry)
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Best Local Similarity 22.27
Matches 55, Conservative
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Gaps

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Indels

32 EFHYTIGPYSTPVLTIEPGDR 52

Conservative

51 HKLKSPLKRILLTHAHGDHIGGLIAVKAAFPEAL. VMIG 48

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92 GAEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGI.:/GTDL.TAMLNDHLPEXVRHIKLIDSE 15.1 1 1 1 1 1 1 1 1 1	152 KVYWSKRHILPYKPHIGTLSVSPEIDSINSLTPUNHGGNMPVPDIGPGSTIYFLVRAPGG 21	212 RLFIGDAHACQGDGEICGTAVEFASITIIKVDLIKNWOLSWPRMENAENIKSIGSARULE 271 1 1 1 1 1 1 1 1 1	272DATRIA 277 201 LFDVTEIA 208
Qy	çy	Qy	Qy
Dio	qa	Db	Db

Search completed: July 3, 2003, 15:47:16 Job time : 84 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw mode:

Run on:
July 3, 2003, 15:45:52 : Search time 25 Seconds
(without alignments)
371.181 Willion only apdates/sec

Perfect score: 1748
Perfect score: 1748
Sequence:
Sequence: 1748
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574
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Minimum DB seq length: C

Maximum DB scq length: 20000c000

Post-processing: Minimum Match 0**

Maximum Match 100**

Listing first 45 summaries

Database: Issued_patents_AA:*

I /cgn2_6/ptodata///iaa/5B_COMB.pep:*

2: /cqn2_6/ptodata///iaa/5B_COMB.pep:*

4: /cgn2_6/ptodata///iaa/AB_COMB.pep:*

5: /cqn2_6/ptodata///iaa/AB_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		i vi	c) i	2	'n	2.	2 2	Sequence 307 App.	42.		Sequence 4, Appli	~	2	23.	.7	•	Ö	(7)	C	-	-	t ~-	÷	Patent No. 5268290
SUMMARIES	US-08-922-865-2 33-69-513-949-2	-08-29	PCT-US95-10661A-6	-08-779-113-2	US-08-583-562B-2	-09-556	US-09-620-412C-180	-08-476-052A-4	4	35-07-976-895-4	3-119-	US-08-475-352-4	5183884-4	-853-2	US-38-914-848-22	-09-413-814-4	US-09-306-446C-2	-08-484	o,	US-08-582-776C-10	-434-831B-	US-09-171-337A-7	8-393	5268290-2
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Score	177.5	9.	, ი	\sim	\sim	82.5	٧.	┰	81.5	81	81	8.1	87	C es		79.5	79	79	79	61.	7	78.5	7.8	78
Result No.	. → 73	3	4 ∙ ∿	ø	۲.	20 C	10	11	12	13	14	1 ເ	16	17	αυ • 1	2.	20	21	22	23	24	25	56	27

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S-08-789-078-2 S-08-752-633-2 S-08-752-633-2 S-08-752-64886-2 S-08-142-623-11 S-08-140-12-623-11 S-08-140-12-623-11 S-08-140-12-623-11 S-08-140-12-623-11 S-08-140-12-63-11 S-08-140-12-63-11 S-08-140-12-63-11 S-08-140-12-9 S-08-150-12-9 S-08-12-9 S-08	MENTS LACTAMASE ENZYME GBTAINED THEIR USE	Veision #1.30 (EPQ)	Gaps 1	DARGYMANNAFIZITANYWY DEGARANDEH DEH LUMIGSALIANDASAEDYALYDDSIYAFET 102 NGPIMYNGAEKGDVLAV	FGG;JGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRHTLPYKPHI 167 	GTLSVSPE
2 US-08-789-078-2 2 US-08-752-633-2 5 PCT-US-6486-7 1 US-08-107-6848-1 1 US-08-107-6848-1 1 US-08-107-6848-2 1 US-09-268-364-2 4 US-09-268-364-2 4 US-09-375-419-9 4 US-09-375-419-9 5 US-09-38-517-9 1 US-08-682-517-9 2 US-08-682-517-9 3 US-08-682-517-9 3 US-08-08-682-517-9 3 US-08-08-682-517-9 3 US-08-08-682-517-9 4 US-08-08-682-517-9 3 US-08-08-682-517-9 3 US-08-08-682-517-9 4 US-08-08-682-517-9 5 US-08-08-682-517-9 6 US-08-08-08-682-517-9 7 US-08-08-08-682-517-9 8 US-08-08-08-08-08-08-08-08-08-08-08-08-08-	ALIGN 5 ISM, AND	-DCS #1.0, 22,865	%; Score 1 %; Pred. N 33; Mism .VLTIEPGDRI	VLAV II LLVVDLLDIGAR	PYGJCAMIPHFGGUJGTDLIAMLNDP 	NATTAHMGQM(
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ωωνννωυφφεφφφφφσασσασσασσασσασσασσασσασσασσασσασσασσασ	TTT quence 2, Application tool 10, 6050616 tool No. 6050616 Event No. 6050616 APPLICANTION TITLE OF INVENTION UNMARK OF SEQUENC COMPUTER READABLE MEDITER READABLE COMPUTER READABLE COMPUTER READABLE COMPUTER READABLE COMPUTER READABLE COMPUTER READABLE COMPUTER READABLE	OPERATING SYSTEM: DESCRIBE PAGENTING SYSTEM: DESCRIBE PAGENTIN CURRENT APPLICATION DAMPER: FILING DATE: FORMATION FOR SEQ ID NESCUENCE CHARACTERISTICATION: SYSTEM STORM TOPOLOGY: Linear TOPOLOGY: Linear MOLECULE TYPE: proteing	ch 1 Similarity 69, Conserv 39 PYSTP	. 60 .		ac m
22222222222222222222222222222222222222	ESULT 1 S-66-922-665-2 S-66-92-665-2 S-66-92-66	CORPOTED SOFTWARE CURRENT APPLICATION FOR FILING DAT INPOSANTION FO SEQUENCE CRACKETT SOFTWARE CRACKET	Query Match Best Local & Matches 39	10 8 ±	113	16 26
	55 7 3. A. C.		9	o de	8 8	රි සි

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RESULT 4
PCI-0895-10661A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 PYGICAMIPH --- - FGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRHTLPYKPHT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 PYSTP------VLTIEPGDRIIVDTRDAFEGAI---NSEQDIPS-QLLKMPFLN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 FIIGMFTKSRHIPGVNFACLIHPGLIGCLPDP----KML-----ASWNERET----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             indeis 101;
                                                                                      TITLE OF INVENTION: MICROORGANISM, LACTAMASE ENZYME OBFAINED TITLE OF INVENTION: THEREFROM, AND THEIR USE NUMBER OF SEQUENCES: 2

COMPUTER REACHBLE FORM:
COMPUTER: IBM PC COMPALIBLE
CORPUTER: IBM PC COMPALIBLE
CORPUTER: IBM PC COMPALIBLE
CORPUTER: PATENTIN PC DOOS/MS-DOS
SOGTWARE: PATENTIN Release #1.0, Version #1.3C (EPQ)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/510,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 SRVFFPVYVDGAGLSVGDLHFSGGDGELTFWGPIEMPGWVHMKVSLLK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 SITYPLVRAPGGRLFLGDAHACQGCGEIC~GTAVEFASITT(KVDL7K 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%; Score 177.5; DB 4; Length 575; 24.0%; Pred. No. 3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08296791
Patent No. 6245337
GENERAL INFORMATION: GENERAL TOPPERSON SERVICENT: St. Gene III, Joseph W. APPLICANT: Falkow, Stanley
ITLE OF INVENTION: Haemophilus Adherence and Penetration
TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/922,865
FILING DATE:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE HARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 PCNGPIMVNGAEKGDVLAV-----
                   : Sequence 2, Application US/09519949
: Patent No. 6423522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 24.0
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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US-C8-296-791-6
US-09-510-949-2
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                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 MYNGAEKGDVLAVY1ESMLPRGVDPY-----GICAMIPHFGGLTGTDLTAMLNDP 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 SINSLIPDNHGGNMDVPDIGPGSIIYP-LVRAPGGRLFIGDAHACQGDGEICGTAVEFAS 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 ILTERDKOGNIJRNWDVGGDNLELVGNAYTYGIAGTPYKVNHENNGLIGFGNSKEFHSDP
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GENERAL INFORMATION:
APPLICANT: Washington University, et al.
TITLE OF INVENTION: Hemophilus Adherence and Penetration Protein
NUMBER OF SECUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.2%; Score 91.5; DB 4; Length 1848; Best Local Similarity 19.1%; Pred. No. 1.4; Matches 73; Conservative 48; Mismatches 127; Indels 135;
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STREET: 4 Embarcadero Center, Suite 3400
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MEDIUM TYPE: Floppy disk
GOMPOTER: IBM PC compatible
GOMPOTER: YSTEM: PC-DCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                       SOFTWARE: Patentim Release #1.0, Version #1.25 CIRRENT APPLICATION DATA:
                                                                                                                                                                                             FILING DATE: 2. CLASSIFICATION: 435
ATTORNEYAGENI INFORMATION:
NAME: Trecartion, Richard F.
REGISTATION NUMBER: 31,801
REPERONE/DOCKET NUMBER: A-59941/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415, 398-3249
TELEPHONE: (416, 388-3249
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 ITTIK---VDLIKNWQLSWPRME-----
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                                                                                                                                           UNBER: US/08/296,791
25-AUG-1994
PC-DCS/MS-DOS
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STATE: California
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                                                                                                                                                      APPLICATION NUMBER:
FILLING DATE: 25-AUG
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193 VPDIGPGSITYPLVRAPGGRLFIGDA#ACQGDGFICG--TAVEFASITIKVDLIKNWQL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 SWPRMENAENIMSIG-SARPLEDATRIAYRDLI-----YW--LVEDFGFEQWDAYM 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKARMI-VDKEYKIGEVDKRIYGS-----FIEHMGR-AVYEGIYEPDHPEADEDGFRKD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08779113
Fatent No. 5948891
GENERAL INFORMATION. Donaid E. APPLICANT: Rarris, Edith S. TITLE OF INVENTION: Cytoplasmic Modulators of Integrin ITLE OF INVENTION: Binding NUMBER OF SOUTHNESS: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Marshall, O'Toole, Gerstein, Murray & 233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MED:UM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,842B
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.7%; Score 82.5; DB 3; 25.4%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Mismatches
                                                                                                                                                                                                                                                N 580-1-009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /product= "abfa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: United States of America
               MEDIUM TYPE: Floppy disk CCMPUTER: IBM PC cCMPatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 LLSQCGKVRLGNMVDPKYTVG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 IKTWC----;GNEMDGPWOIG 181
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLEGINE TWEE: protein:
ORIGINAL SOURCE:
ORGANISM: Bacillus subtilis
                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5860
                                                                                                                                                                                                                                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  500 amino acids
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Best Local Similarity 25.49
Matches 51; Conservative
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  COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 233 SC
CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NAKSHRDVSSEENRYYTVEKNNFPTENVTSFIKERQDAQKRREDYYMPRLDXFVT--EVA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 SINSLIPDNHGGNMDVPDLGPGSITYP-LVRAPGGRLFIGDAHACQGDGEICGTAVEFAS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 PIEASTANNNKGEYNNSD-----KYPAFVRLGSGTQFIYKKGS------RYQL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 ITTIK---VDLIKNWQLSWPRME----------NAENIMSIGSARPLE---DA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 TRIAYRD------GFEGWDAYMLLSO 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 KGILSQDPLINYAVLGDSGSPLFVYDREKGKWLFLGSYDFWAGYNKKSWQEWNIY---- 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 LPEKVRAIKLDSEKVYWSKRHTLP--------YRPHIGTLSVSFEID 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 YTIGPYSTPVLTLEPGD----RIIVDTRDAFE-GAINSE-QDIPSQLLKMPFLNFONGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Score 91.5; DB 5; Length 1848;
/ Pred. No. 1.4;
48; Mismatches 127; Indels 135; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SarNo. SarNo. SarNo. SarNo. Tacher Sarno. Tacher Sarno. Sarno. Title OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGIUS GENETITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/266,791
FILING DATE: 25-AUG-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31.691
REFERENCE/DOCKET NUMBER: FP-59941/RFT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 MVNGAEKGDVLAVYIESMLPRGVDPY-----
             JMBER: PCT/US95/10661A
16-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 CGKVRLGNMVDPKYTVGAMLNKN 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 --KHEFAEKIYOOYSAGSI,IGSN 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64, Application US/08926942B Patent No. 6030807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                          1848 amino acids
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Best Local Similarity 19.1.
Hest Cocal Similarity 19.1.
CURRENT APPLICATION DATA:
               APPLICATION NUMBER:
FILING DATE: 16-AUG
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                                                           CLASSIFICATION:
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US-08-926-842B-64
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                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY
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13;

Gaps

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Sequence 180, Application US/09556877
Patent No. 6432916
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 SEQUENCE CHARACTERISTICS: LENGTH: 858 amino acids TYPE: amino acid TOPCHOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 ----KGDVL----
                                                                       CS-08-583-562B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probst, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Probst,
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US-09-556-877-180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 LAVYIESMLPRGVDPYGICAMIPHFGGLTGTDL - TAMLNDPLPEKVRMIKLDSEKVYWS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 ------IIVDTRDAFEGAINSEQDIPSQLLKMPFLNPQNGPIMVNGAEKGDV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 KRHTLPYKPHIGTLSVSPETDSINSLIPDNHGGNMDVPDIGPGSLTYPLVRAPGGRL 213
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                                                                                                                                                                                                                                                                                                                                                                    73;
                                                                                                                                                                                                                                                                                                                                 Query Match 4.7%; Score 82.5; DB 2; Length 857; Best Local Similarity 26.3%; Pred. No. 4.3; Matches 48; Conservative 31; Mismatches 85; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Marshall, O'foole, Gorstein, Murray & Borun
233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08583562B
Patent No. 5922570
GENERAL INFORMATION:
APPLICANT: Stannton, Donald
APPLICANT: Harris, Edith
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                              REFERENCE/DOCKET NUMBER: 35,802
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-474-630
TELEFAX: 312-474-648
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/33033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/583,562B
APPLICATION NUMBER: US/08/779,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   ATTORNEY/AGENT INFORMATION:
NAME: Greta E. No. 5948891and
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZiF: 0000CC
COMPUTER FEACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                       857 amino acids
amino acid
                                                                                                                                                                                                                                                              not relevant
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                                                                                                                                                                                                                                                                   MOLECULE IYPE: protein
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                                    CLASSIFICATION:
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US-09-583-562B-2
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234 DEPCLEKREPNNHIGISFIPREVGEHLVSIKKNGNHVANSPVSIMVVQSEIGDARRAKVY 263
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                                                                                                                                                                                                                                                                                                                                                                                                                           99 I.AVYIESMLPRGVDPYGICAMIPHFGGLIGTDL--TAMLNDPLPEKVRMIKLDSEKVYWS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 QTEDLED-----GTC-KVSYFPTVPGVYIVSIKFADEHVPGSPF1VKISGEG---- 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 LTAMLNUPLPEKVRMIKLDSEKVYWSKRHTLPYKPHIGTLSVSPEIDSINSLTPDNHGGN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 L------EEIR-IKYNKAGTPETKKITL---PSLKAQASAGNADAWASSSPQSGSGA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 KRHTLPYKPHIGTLSVSPEIDSINSLTPDNHGGNMDVPDIGPGSITYPLVRAPGGRL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 -----RVKESITRTSRAPSVATVGSIC----DLNLKIPEINSSDMS-AHVTSPSGRV 395
                                                                                                                                                                                                                                                                                   53 .....IVDTRDAFEGAINSEQDIPSQILKMPFLNPQNGPIMVNGAEKGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4C YSTPVLT1EPGDRIIVDTRDAFE - GAINSEQDIPSQLLKMPFLNPQNGPIMVNGAE - - -
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                                                                                                                                           5 EESIMAKR-----GVGAGRKPVTHHLTEEMQKEFHYTIGPYSTPVLTIEPGDR-----
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77;
                                                                         Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fling, Steve
APPLICANT: Fling, Steve
APPLICANT: Maisonneave, Jeff
APPLICANT: Maisonneave, Jeff
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-64-19
NUMBER OF SEO ID NOS: 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1752;
       Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                         85;
Unery Match 4.7%; Score 82.5; DB 2; Best Local Similarity 20.3%; Pred. No. 4.3; Matches 48; Conservative 31; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cuery Match 4.7%; Score 82.5; DB 4; Best Local Similarity 23.1%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 MDVPDIGPGSI-----TYPLVRAPGGRLF 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 3.0/4.0
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524 HLLSCGLDNTIKLWDVKTGKCIRTQFG-----HVEGVWDIAADNFRIISGSHDGSIKVW 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTMARE: EstastEG (for Windows Version 2.0
COMPUTER: OF JUN 1995
FILING DATE: OF JUN 1995
FILING DATE: OF JUN 1995
FILING DATE: 21-MAR.1954
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN.1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN.1990
APPLICATION NUMBER: 07/539,842
FILING DATE: 28-JUN.1981
APPLICATION NUMBER: 07/539,842
FILING DATE: 28-JUN.1981
APPLICATION NUMBER: 07/539,842
FILING DATE: 28-JUN.1981
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00785/068003
                                                                                                                                                                                                                                                                           Segmence 42, Application US/08476062A Patent No. 5877275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPRONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1170 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suery Match
Best Local Similarity 22.7%
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 0210-2804
COMPUTER REGARLE FORM:
MEDIUM TYPE: Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Freeman, John W. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                             240 IKVDI, 244
                                                                                                                                                                   634 YKFDL 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIREET: 225 E
CITY: Boston
                                                                                                                                                                                                                                     RESULT 11
US-08-476-052A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 GAIYAKGDLSIOSSKQSLFNSNYSKQGGGALYVE------GGINFQD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13. LTAMLNDPLPEKVRMIKLDSEKVYWSKRHTLPYKPHIGTLSVSPETDSINSLTPONHGGN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 NPQNGPIMVNGAEKGDVLAVYIESMLPRGVDPYGICAM:PHPGGLTGTDGTAHGNPPLPE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 KVRMIKLDSEKVYWSKRHTLPYKPHIGTLSVSPEIDSINSLIPJN-----HGGNMOVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 L------EEIR-IKYNKAGTFETKKITL---PSLKAQASAGNADAWASSPGSGSGA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: TYEES MIKE
APPLICANT: TYEES MIKE
APPLICANT: TYEES MIKE
APPLICANT: Willems, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIOUTIN
TITLE OF INVENTION: DEPENDENT PROTECLYSIS
FILE REFERENCE: 11757.103501
CURRENT APPLICATION NUMBER: 60/292,443
PRIOR PELICATION NUMBER: 60/292,443
PRIOR FILLING DATE: 1998-10-23
PRIOR FILLING DATE: 1998-07-10
PRIOR FILLING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 SPQDDPTWTDGADESDTPSNEQSTVCDE-----NLPVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 YSTPVLTIEPGDRIIVDTRDAFE--GAINSEQDIPSQLLKMPFLNPGNGPIMVKGAE---
                                                                                                                                                                                                                                                                                                                                                                                  4.7%; Score 82.5; DB 4; Lonath 1752; 23.1%; Pred. No. 14; tive 26; Mismatches 60; Indels 77
                                                            GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREAIMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620.412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ fOF Windows Version: 3.6/4.5
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21.1%; Pred. No.
                      Sequence 180, Application US/09620412C
Patent No. 6448234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 30, Application US/09177165A Patent No. 6426205
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Matches 39; Conserv
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Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                   ORGANISM: Chlamydia
  US-09-52C-412C-180
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US-09-177-165A-30
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LENGIH: 175
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284 GIGK----HFCTKESOETLHKFASKPASE------FVKILDTFE-----318
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                                    73 SQLLKMPFLNPQNGPIMVNGAEKGDVLAVYIE-----SMLPRGVDPYGICAMIPHFGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 VGAGRKPVTHHLIEEMQKEFH-YTIGPYSTPVLTIEPGDRIIVDTRDAFEGAINSEQDIP
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Arnaout, M. Amin
TITLE OF INVENTION: CONINGLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETAZ INTEGRINS
NIMBER OF SEQUENCES: 53
GORRESSED MODRESSE: 718h & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.7%; Score 81.5; DB 2; Length 1170:
22.7%; Pred. No. 9.4;
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Sequence 4, Application US/07978895
Patent No. 5480568
GENERAL INFORMATION:
APPLICANT: REAUS. Matthias H.
APPLICANT: Aaronson, Stuart A.
TITLE OF INVENTION: BPIDERMAL GROWTH FACTOR RECEPTOR, ANTIGEN THERETO, AND
TITLE OF INVENTION: BIOASSAYS AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1030 ALSLPVGTLNRPRGSQSfJSPSSGYMPMNQGNLGESCQ····ESAVSGSSEKCPRPVSLHP 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    978 IKRESGPGIAPGPEPHGLINKKLEEVE--LEPELDLDLDLEAEEDNLATT-----TLGS 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 EQDIPSQLLKMP----FLNPQNGPIMVNGAEKGDVLAVYIESML-----PRGVD--- 112
                                                                            134 LLFQEPQGGCHWSQVQT1HGTQTGSYFGGELCCVDVDQDGETELLIGAPLFYGEQRGGR 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 -PYGICAMIPHFGGLIGIDLTAMLNDPLPEKVRMIKLDS------EKVYWSKRHTL- 161
                                                                                                                                                                  988 CV.TDGDGLVD 538
377 F - IDEKADIÇEDIFFIGNEPLIFEVRAĞYL-GYTVIWLPSKQKTSLLASĞAPRYQHMĞRV 433
                                                                                                                          213 LFT-----GDAHACQGD-GEICGTAVEFASITTIKVDLIKNWQLSWPRMENAENIMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
                                        171 SVSPE-----IDSINSLIPENH-GGNMENPDIG-PGSITYPLVRAP---
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                                                                                                                                                                  494 VETYQRRQLGFEEVSELQCDPGYPLG---RFGEALTALTDI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENT Release #1.0, Version #1.25
CURRUT APPLICATION DATA:
APPLICATION NUMBER: US/07/978,895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.6%; Score 81;
24.6%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19921110
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,406
FILING DATE: 01-0EC-1989
ALIGENEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/POCKET NUMBER: 1414-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (464) 688-0776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Suite 400
STREET: 133 Carnegie Way, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33,438
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Perryman, David G
RECISTRATION NUMBER: 33
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Best Local Similarity 24.6%
Matches 52; Conservative
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// MOLECULE TYPE: protein
US-07-978-895-4
                                                                                                                                                                                                           IGSARPLED 272
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539 VAVGAPLEE 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                        RESULT 13
US-07-976-895-4
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--- LPYKPHIGHL 170
                                        377 F.-LDEKABLODDIFIGNEPHIPBVRAGYL-GYTVIWLPSROKISTLASSAPRYDHGSRY 433
                                                                                                                   134 LLEQEPQGGGHWSQVQTIRGTQIGSYFGGELGGVDVQQDGETELLIGGAPJFYGFJRGGG 494
                                                                                                                                                                     213 LFI------GDAHACOGD-GELCGIAVEFASITTIKVDLIKNWOLSWFRMENAENIMS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
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                                                                                                                                                                                                       194 VFIYQRRQLGFEEVSELQGDPGYPLG---REGRAITALTDI------NGDGLVD
                                                                                   SVSPE-----IDSINSLTPDNH-GGNMDVPDIG-PGSLTYPLVRAP----GGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5: Length 1170;
.26 LIGIDLIAML-----SKRHT---SKRHT-
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 42, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Annaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Mismatches 109;
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Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.9)
SOFTWARE: MordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 50786/267001
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
PCILNG DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (617) 542-8906
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Best Local Similarity 22.70,
Best Local Similarity 22.70,
Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: John W. Freeman
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
                                                                                                                                                                                                                                                      264 IGSARPLED 272
                                                                                                                                                                                                                                                                                               539 VAVGAPLEE 547
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02110-2804
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PCT-US96-01314-42
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US-08-475-352-4

Sequence 4, Application US/08475352

Sequence 4, Application US/08475352

Sequence 4, Application US/08475352

GENERAL INFORMATION:
APPLICANT: Kraus, Matthias H.
APPLICANT: AARCGOON, Stuart A.
APPLICANT: ASCIGNATION: AN ISOLATED POLYPEPTIDE RELATED TO THE TITLE OF INVENTION: BIOSCHAPE PROTOR RECEPTOR, ANTIGEN THERETO, NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         978 IKRESGPGIAPGPEPHGLTNKKLEEVE--LEPELDLDLDLDEABEDNLATT-----TLGS 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1030 ALSLPVGTLNRPRGSQSLLSPSSGYMPMNQGNLGESCQ---ESAVSGSSERCPRPVSLHP 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1087 MPRGCLASESSEGHVTGSEA-----ELQEKVSMCRSRSRSRSPRPRGDSAYHSORHSLL 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1141 TPVTP-----LSFPGLEEEDVNGYVMPDTH 1165
1141 IPVTP-----LSPPGLEEEDVNGYVMPDTH 1165
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24.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/444,436
Fliing Date: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
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Job time : 38 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/475,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION DATA: APPLICATION NUMBER: 07/978,895
                                                                                                                                                                                                                                                                                                               5: Suite 400
133 Carnegie Way, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (404) 688-9880 HYDRMATION FOR SEQ 1D NO: 4 SEGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 24.6
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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INFORMATION FOR
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STREET: 13
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APPLICANT: AARONSON, Stuart A.
TITLE OF INVENTION: AN ISOLATED POLYPEPTIDE RELATED TO THE
TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR, ANTISEN THERETO, AND
TITLE OF INVENTION: BIOASSAYS AND METHODS RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1030 ALSEPVGTLNRPRGSQSLISPSSGYMPMNQGNLGESCQ---ESAVSGSSERCPRPVSLHP 1066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79;
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                                                                                          1141 IPVTP-----LSPPGLEEEDVNGYVMPDTH 1165
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                                                           162 -PYKPHIGTLSVSP---EIDSINS-LIPDNH 187
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24.5%; Pred. No.
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FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/979,895
FILING DATE: 10-NOV-1992
APPLICATION NUMBER: US 07/444,4
                                                                                                                                                                                                                                                                                                                                                                                                                                      133 Carnegie Way, N.W.
                                                                                                                                                                                                          : Sequence 4, Application US/68473119
; Patent No. 5820859
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REPERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMERIUM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
TNFORMATION FOR SEQ ID NO: 4:
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Best Local Similarity 24.58
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     Suite 400
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MEDIUM TYPE: Floppy
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GenCore version 5.1.6
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OM protein – pr	OM protein - protein search, using sw model
Run on:	<pre>July 3, 2003, 15:48:47 ; Search time 53 Seconds</pre>
Title: Perfect score: Sequence:	US-10-085-082-2 1748 1 MKWLEESIMAKRGVGAGRKPGNMVDPKYTVGAMLNKNLLV 328
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	440863 segs. 114992915 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Natch 160% Listing first 45 summaries

Database

/gran__//producta///pubpaa/USOG__MEM__//producta///pubpaa/USOG__MEM__//pubpaa/USOG__MEM__//pubpaa/USOG__MEM__//pubpaa/USOG__MEM__//pubpaa/USOG__MEM__//pubpaa/USOG__MEM__//pubpaa/USOG__MEM__//pubpaa/USOG__MEM__//pubpaa/USOG__MEM__//puppaa/USOG__MEM__//puppaa/USOG__MEM__//puppaa/USOG__MEM__//puppaa/USOG__MEM__//pop.* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result.	Score	Query Match	Query Match Length DB	DB	ID	Description
	1748	100.0	328	6	US-10-C86-082-2	Sequence 2, Appli
7	161	9.5	416	ø,	US-10-156-761-9482	Sequence 3482. Ap
٣	148	8.5	33	ᠬ	US-10-086-082-14	Sequence 14, App.
7	117	6.7	21	c)	US-10-686-082-11	Sequence 11, Appl
ហ	101	S. S.	525	Ċ	US-10-004-551-18	Sequence 18, Appl
9	101	5.8	525	φ	US-10-004-551-20	Sequence 20, Apri
7	101	5.8	525	ტ.	35-10-004-551-22	Serucace 22, Appl
пo	101	5.8	526	ന	US-10-C04-551-24	24.
6	:01	5. 39	866		US-10-004-551-14	Sequence 14. Appl
10	101	5.8	994	2	CS-10-004-551-16	Sequence 16, Appl
11	100.5	5.7	261	œ	US-10-004-551-26	26,
12	100	5.7	23	ಭ	US-10-086-082-12	Sequence 12. Appl
13	66	5.7	20	6.	HS-10-085-082-3	Sequence 1, Appli
14	8.6	5.6	18	ď.	US-10-086-082-9	Sequence 9. Appli
15	96	5.5	1094	σ	08-10-156-761-11435	Sequence 11435, A
16	† *6	5.4	19	0	US-10-086-082-1C	Sequence 10, Appl
17	93	5.3	682	10	US-09-798-791-2	Sequence 2, Appl:
18	92.5	5.3	381	c	US-10-128-714-8002	Segmence 9002, Ap
19	91.5	5.2	1848	6	CS-08-839-996-6	Sequence 6, Appli

4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	sequence 0044, Ap Sequence 189, App Sequence 11162, A Sequence 1, Appli Sequence 11791, A
0.080	0.S-09-7.88-c.26-684 10 0.S-09-841-7.32-389 9 0.S-10-156-761-11162 9 0.S-10-007-706-1
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APPLICANT: Rinder, Andrew
APPLICANT: Rebins, Karen
APPLICANT: Robins, Karen
APPLICANT: Shaw, Nicholas
APPLICANT: Linschert, Andreas
APPLICANT: Zimmermann, Thomas
APPLICANT: Zimmermann, Thomas
APPLICANT: Andreas
APPL
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100.0%; Pred. No. 5e-163;
ative 0; Mismatches 0;
                                Sequence 2, Application US/10086092 Publication No. US20036087402A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Klebsiella oxytoca
US-10-086-082-2
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Hest Local Similarity 100.
Matches 328, Conservative
10-086-082-2
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US-10-086-082-14
Sequence 14, Application US/10086082
Fublication No. US20030087462A1
GENERAL INFORMATION, Walter
APPLICANT: Brieden, Walter
APPLICANT: Robins, Karen
APPLICANT: Shaw, Nicholas
APPLICANT: Shaw, Nicholas
APPLICANT: Linschert, Andreas
APPLICANT: Zimmermann, Thomas
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87.9%;
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Bost Local Similarity 87.9
Matches 29; Conservative
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LENGIH: 33
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TYPE: PRT
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                                                                             44 VLIIEFGDRIIVDTRDAFE---GAINSEQDIPSQLLKMPFLNPQNGP!XVNGAEKGDVLA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 VDII.DI.GPVPQQTGDAAGQGWGYTGIFAKANGGGFI.TDYFPDAYKAVWDFHGQQAVSRHI.
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                           262 MSIGSARPLE-----DATRIAYRDLIYWINE---DFGFEGWDAYMLE-SQCGKVKLGNWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TILLE OF INVENTION: NOVEL POLYNJCLEDIIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
SPIOR FILING DATE: 2001-08-02
NUMBER OF SEO ID NOS: 15109
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301 SOCGRVRLGNMVDPRYTVGAMLNRNLEV 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptomyces avermitiiis US-10-156-761-9482
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US-10-156-761-9482
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Best Local :
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FILLE REFERENCE: 32213
CURRENT APPLICATION UNBER: 2062-28
PRIOR APPLICATION NUMBER: US/09/214,679
PRIOR FILING DATE: 1999:12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
TITLE OF INVENTION: METHOD OF PREPARING (S)-OR (R)
TITLE OF INVENTION: -3,3,3,7-TRIFLUORO-2-HYDROXY-2-METHYLPROPIONIC ACID
FILE REPERFNCE: 32213
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100.0%; Pred. No. 7.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 148; DB 9;
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 GVDPYGICAMIPHFGGLTGTDLTAMINDPLPEK 142
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                                                                             CURRENT APPLICATION NUMBER: US/10/086,082
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US/09/214,679
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20030087402A1
GENERAL INFORMATION:
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Query Match
Best Local Si
Matches 60,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 WTPTQEGPGDMGRPWVAEVVSQGAGIGIQGIIISSTASGDBEITTTTTTTTTTTTVQT 240
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(2)
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                GENERAL INFORMATION:
APPLICANT: SHIKERS, RICHARD A
APPLICANT: SHIKERS, RICHARD A
APPLICANT: SHIKERS, RICHARD
IITLE OF INVENTION: POLYNUCLEOTIDES AND POLYFFPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ. ID NOS: 11
SOFTWARE: PALCALLIN VEY: 2.1
SSCTWARE: PALCALLIN VEY: 2.1
LENGTH SES
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APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES FINCODED THEREBY
FILE REFERENCE: 15966-559
CORRENT APPLICATION NOWBER: US/10/004,551
CORRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
RIUMBER OF SED ID NOS: 11C
SOFTWARE: PATENTIN VET. 2.1
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Live 28; Mismatches 105;
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23.9%; Pred. No. 0.25;
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COTHER INFORMATION: 0.2077 can be A. G. C. or T.
US-10-004-551-20
                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
COTHER INFORMATION: n 2077 can be A. G. C. or T.
US-10-004-551-18
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Publication No. US20030004310A:
GENERAL INFORMATION:
Publication No. US20030004310A1
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Best Local Similarity 23.99
Matches 60: Conservative
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Matches 60; Conservative
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US-10-004-551-20
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LENGTH: 525
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181 WIFTQEGPGDMGRPWV&VSQGAGIGIQGIIISSTASGDDEETITITTITITTITITVQT 240
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96 GDVLAVYIESMI.PRGVDPYGICAMIPHFGGLTGTDLIAMLNDPLPERVRMIKLDSEKVYW 155
                                                                                                 156 SKRHTL---PYKPHIGTLSVSPEIDS--INSLTPDNHGGNMDVPDIGPGSI--TYPLVRA 208
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APPLICANT: SHIMKETS, RTCHARD A
APPLICANT: SHIMKETS, RTCHARD A
APPLICANT: FERNANDES, ELMA
ITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REPREHENT
CURRENT APPLICATION NUMBER: US/10/C04,551
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR APPLICATION NUMBER: 09/635,949
SRICH RILING DATE: 2000-08-10
NUMPER: CF SEQ ID NOS: 116
SSCIEN NO 22
LENGTH: 525
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FUBLICATION NO. US20030004310A1
APPLICATIN SHIMKETS, RICHARD A
APPLICANT: SHIMKETS, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
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Pred. No. 0.26;
8: Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 22, Application US/10004551; Publication No. US20030004310A1; GENERAL INFORMATION:
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||Similarity 23.9%;
|50; Conservation
                                               GD---EELKPALPFOPDP--
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US-10-004-551-24
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156 SKRHTL---PYKPHIGTLSVSPEIDS--INSLTPDNHGGNMDVPDIGPGSI--TYPLVRA 208
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                                                                                                         96 GDVLAVYIESMLPRGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYW 155
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                     121 SPTPAMAAVPTOPOSKEGPWSPESESPMIRITAPLPPGFSMAVPTLGPGEIASTTPPSRA 180
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                                                                      209 -----pG--GRLFIGD------AHACQGDGE--ICGTAVEFASITIKV
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Fibilication No. US20050064310A1
GENERAL INFORMATION
AFPLICANT: SHIWKIS.
HERBARDS, ELMA
ITTLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-55
PRIOR FILILGATION UMBER: 09/635,949
FRIOR FILING DATE: 2000-00-10
NUMBER OF SEQ ID NOS: 110
                                                                                                                                                                                                                                                                                                                                                  Sequence 16. Application US/10004551
publication No. US2003C004316A.
GENERALINFORMATION:
APPLICANT: SHIMMEDS, ELMA
APPLICANT: FERNANDES, ELMA
APPLICANT: FERNANDES, ELMA
APPLICANT: FERNANDES, ELMA
APPLICANT: FOLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE PEFERENCE: 15966-559
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR PILING DATE: 2000-08-10
NUMBER: 0F SEQ ID NOS: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 101; DB 9; Length 994;
23.9%; Pred. No. 0.65;
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CTHER INFORMATION: n 1755 can be A. G. C. or T.
US-10-004-551-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 23.9%
Matches 60; Conservative
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0S-10-004-551-26
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TS-16-904-551-16
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US-10-004-551-14

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US-10-004-551-14

Sequence 14. Application US/10064551

Publication No. US20030004310A1

GENERAL INFORMATION:
APPLICANT: SHIMKETS, RICHARD A
APPLICANT: PERNANDES, ELMA

1717LE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REPERENCE: 15966-559
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Best Local Similarity 23.9%; Pred. No. 0.26;
Matches 60; Conservative 28; Mismatches 185; Indels
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23.9%; Pred. No. 0.65;
tive 28; Mismatches 105;
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OTHER INFORMATION: n 1755 can be A. G. C. or T
US-10-004-551-14
                                                                                                                                                                                                     : TYPE: PRT
ORGAN:SM: Homo sapiens
CTHEN INFORMATION: n 2093 can be A. G. C. or
US-10-004-551-24
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CURRENT FILING DATE: 2001-12-35
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 11C
SOFTWARE: Patentin Ver: 2.1
CURRENT APPLICATION NUMBER: 08/10/004,551
                  CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2006-10-10
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentle Ver: 2.1
SLENGTH: 526
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Best Local Similarity 23.39
Matches 60; Conservative
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LENGTH: 993
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Naughton, Andrew
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Sest Local Similarity
Matches 19; Conserv
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US-10-086-082:9
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LENGTH: 20
   APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 12, Application US/10086082

Publication No. US20030087462A1

GENERAL INFORMATION:
APPLICANT: Brieden, Walter
APPLICANT: Robins, Marce
APPLICANT: Timechert, Andreas
APPLICANT: Zimechann, Thomas
APPLICANT: Zimechann, Thomas
APPLICANT: Zimechann, Thomas
APPLICANT: Zimechann, Thomas
APPLICANT: Slaw, Nicholas
APPLICANT: Zimechann, Thomas
APPLICANT: Slaw, Nicholas
APPLICANT: Slaw, Ni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 SKRHTL---PYKPHIGTLSVSPBIDS--INSLIPBNHGGNMDVPDIGDGSI--TYPLVRA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 ------PG--GRLFIGD--------AHACQCDGE--ICGTAVEFASITTIKV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 WIPPOEGPGDMGRPWVAEVVSQGAGIGIOGTHISSIASGDDEETHITTTIJJTTTTTTTTVGT 240
                                                                                                                                                                                                                                                                                                                                                                          36 TIGPYSTPVLTIEPGDRIIVDTRDAFEGAINSEQDIFSQLLKMPFLNPGNGPIMVNGABK
                                                                                                                                                                                                                                                                                                                                                                                                                                          26 IVGKGGAPGIBETDGELTAAPTPEQPERGVHFVTTAPT--LKLLNHHPLLBEFLQBSLEK
                                                                                                                                                                                                                                                                                                             63; Gaps
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                                                                                                                                                                                                                                                Length 261:
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ilarity 91.3%; Pred, No. 0.6038;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                         Ouery Match 5.7%; Score 100.5; EB 9; Best Local Similarity 23.3%; Pred. No. 6.11: Matches 66; Conservative 31; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 LF1GDAHACQGDGEIGGTAVEFA 235
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Publication No. US20030087402Al
GENERAL INFORMATION: APPLICANT: Brieden, Walter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 D----LIKNWOLSWPRM 255
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SOFTWARE: PatentI: Ver. 2.1
SEQ ID NO 26
LENGTH: 261
TYPE: PAT
                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-004-551-26
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Best Local Similarity
Matches 21; Conserv
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Publication No. US20030387402A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Brieden, Walter
APPLICANT: Robins, Karon
APPLICANT: Tinschert, Andreas
APPLICANT: Zismermann, Thomas
TITLE OF INVENTION: HELHOO OF PREPARING (S)-OR (R)
TITLE OF INVENTION: HELHOO OF PREPARING
TITLE OF INVENTION: A3.3-TRIFLUORO-2-HYDROXY-2-METHYLPROPIUMIC ACID
FILE KEPERENGE: 32213
CURRENT APPLICATION NUMBER: US/09/214,679
PRIOR APPLICATION NUMBER: US/09/214,679
PRIOR FILING DATE: 1999-12-30
NYMBER OF SEV ID NOS: i4
SOFTWARE: FASTER FOR MINDOWS VERSION 3.0
APPLICANT: Robins, Karen
APPLICANT: Robins, Karen
APPLICANT: Tinschert, Andreas
APPLICANT: Tinschert, Andreas
APPLICANT: Zimmermann, Thomas
APPLICANT: Zimmermann, Thomas
APPLICANT: Zimmermann, Thomas
TITLE OF INVENTION: HETHON OF PREPARING (S)-OR (R)
TILLE OF INVENTION: -3,3,3-TRIFILUORO-2-HYDROXY-2-METHYLPROPIONIC ACID
COURENT APPLICATION NUMBER: US/10/086,682
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 1999-12-30
KNARER OF SEQ ID NOS: 14
SOFIWARE: FESTSEQ for Windows Version 3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 99; DB 9;
95.0%; Pred, No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKWLEBSIMAKRGVGAGRKP 20
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: ORGANISM: Klebsiella oxytuca
US-10-086-082-9
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HORIKAWA, HIROSHI
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US-10-066-682-3
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383 VERAADAYAGILAAWRPVIPGI-----IGLVPGPLGKGVLDGALKÇAILDRLPRTAFL 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 VYIESMLPRGVD-----PYGICAMIPHFGGLIGTDLTAMINDPIPERV-RMIKLDSEKV 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.5%; Score 96; DB 9; Length 1094;
21.9%; Pred. No. 2.3;
Arive 35; Mismatches 118; Indels 118; Gaps
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKKI, VOSHIYUKI
APPLICANT: HATTONI, MASHIYUKI
TILE OF INVENTION: NOVEL POLYNUCLEDITORS
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-55-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
PRIOR FILING DATE: 2001-06-03
PRIOR FILING DATE: 2001-06-03
PRIOR FILING DATE: 2001-06-03
NUMBER OF SEQ ID NOS: 15109
SEG ID NO 11435
LENTH: 1094
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US-10-156-761-11435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuery Match
Best Local Similarity 21.9%
Matches 76; Conservative
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Search completed: July 3, 2003, 15:58:52 Job time: 54 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compagen Ltd.

protein - protein search, using sw model ω O

July 3, 2003, 15:42:52 ; Search time 41 Seconds kun on:

(without alignments)
769.075 Million cell updates/sec

US-10-086-082-2 1748

1 MKWLEESIMAKRGVGAGRKP......GNMVDPKYTVGAMLNKNILV 328 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

28 1224 of hits satisfying chosen parameters: Potal number

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 169% Listing first 45 summaries

PIR_73:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical proto-probable acetamida-amidase-related prote-hypothetical prote-hypothetical prote-hypothetical prote-formanidase. Like p-formanidase. Like p-formanidase. Like p-formanidase. Like p-formanidase. Like pprobable formamida formamidase (EC 3. hypothetical prote acetamidase - Myco acetamidase - Myco probable formamida hypothetical prote hypothetical prote lacz expression re cytochrome P450 ib T518.5 protein - A alpha-L-arabinofur excinuclease ABC c amidase (EC 3.5.1, excinuclease ABC c inactivated probab hypothetical prote acetamidase BH0025 probable multifunc cell division prot nitrate reductase Description SUMMARIES S74034 A81138 H96927 A83653 B90458 B90458 B90458 B90458 B90458 C72424 C72424 C72424 A31776 A317776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A317776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A317776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A317776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A317776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A317776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A317776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A31776 A317776 A317776 A317776 A317776 A317776 A31776 A317776 A3177 AC1861 G75582 DB Length Query Match 1 Score Š. Kesult

hypothetical protein SSG2810 (imported) - Suifolobus solfataricus C:Species: Sulfolobus solfataricus C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 B:She, Q: Sindh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; C Jong, I.: Jeffries, A.C.: Kozera, C.J.: Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redde

RESULT 2 B90458

to the mypothetical fab/FMN containing hypothetical protein intrate reductase protein F53H1.4 [1] IgA-specific metal acctate COA ligase hypothetical protein actin - Cryptospor	889386 897386 686856 686433 686433 641859 641859 845634	200200000	428 467 773 868 1378 1849 552 1661	. w w w w w w w 4 . u o o o o o o o o	888 888 88 8 1 1 1 1 1 1 1 1 1 1 1 1 1
fAD/FMN-containing	B97213	~	467	5.1	88.5
CI648 hypothetical	B86586	7	428	5.1	in.
conserved hypothet	672037	~	428	5.1	86.5
polynucleotide pho	683950	~	704	5.1	90 O
aldehyde dehydroge	C69584	~	485	5.1	ۍ ص
polyphosphate kina	G85893	~	689	5.1	r.
polyphosphate kina	C91049	c٦	688	5.1	89.5
polyphosphate kina	A443C6	7	688	5.1	89.5
probable ABC trans	E95356	~	491	5.1	90

ALIGNMENTS

##857L1 1 ##857L1 1 ##857L1 1 ##867L1 1 ##867L
HESTL! 1 A8363 acctandase BH acctandase BC C.Dato: 01-Dec C.Dato:

0.5 SKRHTLPYKPHIGTLSYSP	OV 276 IAYRDLIYWJUEDFGFEGWARMILSQCGKVRLGNMVD-PRYTUGAMINKNLLU 328 11	##SSUIT 4 ##SSUIT 5 ##SPECIOS: Caulobacter crescentus C:Specios: Caulobacter crescentus R:Nierman, W.C.: Feldblyum, T.V.: Paulsen, I.T.: Nelson, K.E.: Eisen, J.: Heidelberg, R:Nierman, W.C.: Feldblyum, T.V.: Paulsen, I.T.: Nelson, K.E.: Eisen, J.: Heidelberg, R:I. Laub, M.I.: DeBoy, R.T.: Dodson, R.J.: Durkin, A.S.: Gwinn, M.L.: Haft, D.H.: Kc C: Translaeva, M.: White, O.; Salzberg, S.L.: Shapiro, I.; Venter, J.C.: Fraser, C R:I. Complete Genome Sequence of Caulobacter crescentus. A:Reference number: A87249; MuID:21173698; PMID:11259647 A:Reference number: A87249; MuID:21173698; PMID:11259647 A:Residues: 1-304 <stoa 1-304="" <stoa="" a:residues:="" c25011="" c25011<="" th=""><th>Agrones 99; Qy 43 PVL Db 8 PVL 1 J 8 PVL Oy 90 VNG 1 J 65 IAG 1 J 7 PVL Oy 203 YPL Oy 256 ENA Oy 256 ENA</th><th>Cy 316 YIVGAMLNKNLL 327 DD 292 KGVHALLSKGLL 303 RESULT 5 E75139 Lypotherical protein PAR0614 - Pyrococcus abyssi (strain Orsay)</th><th>a.</th></stoa>	Agrones 99; Qy 43 PVL Db 8 PVL 1 J 8 PVL Oy 90 VNG 1 J 65 IAG 1 J 7 PVL Oy 203 YPL Oy 256 ENA Oy 256 ENA	Cy 316 YIVGAMLNKNLL 327 DD 292 KGVHALLSKGLL 303 RESULT 5 E75139 Lypotherical protein PAR0614 - Pyrococcus abyssi (strain Orsay)	a.
arrett, R.A.: Ragan, M.A.; Senser, C.W.; Van der Cost. J. submitted to GenBank, April 2021 A:Description: Shifo.chus solfataricus complete genome. A:Reference number: A99139 A:Accession: B9438 A:Accession: B9438 A:Accession: B9438 A:Actus: preliminary A:Molecule type: DNA A:Residues: 1-318 < KUK> A:Cross-references: GB:AE006541: NID:G13816160; FIEN:AAK42921.1; GSP)B:GNTG155 C:Genctics: A:Gene: SSC2810	Cuery Match Best Local Similarity 35.0%; Pred. No. 7e-21; Matches 106; Conservative 49; Mismatches 118; Indels 30; Gaps 11;	43 PVLIEBGDRIIVDIRDAPRBAINSEODIPSGLDKWEFIMPONDHIMWNGARKEE FILL FILL FILL FILL FILL FILL FILL FI	to K1) S.: Baikawa, Y.: Jibruo, K.: uka, T.: Kudoh, Y.: Yamazaki thetmophilic Crenarchaeon, 566 SwA79455.1: Pibrig5104179		96 GDVLAVYIESMLPRGVDPYGICAMIPHFGGLIGTDLTAMLNOPDPERVRAHKJOSEKVVW 155 1651 1 1 1 1 1 1 1 1 1

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hypothetical protein all0706 [imported] - Nostoc sp. (strain PCC 7120)
Cispecies: Nostoc sp.
Cispecies: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
Cispecies: All084
Cispecies: 14-Dec-2001 *sequence_revision 14-Dec-2001 *text_change 30-Jun-2002
Cispecies: nath894
Rixaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irig
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabat
DNA Ros. 8, 265-213, 2001
A;Fillo: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807: MUID:21595285; PRID:11759840
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C.Species: Listeria innocua
C.Daceles: Listeria innocua
C.Date: 27-Nov-2001 #Sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C.Accession: AB1776
R.Giaser, P.: Frangeul, L.: Buchrieser, C.: Amend, A.: Baquero, F.: Berche, P.: Bloe
D.: Dominquez-Bernal, G.: Duchaud, E.: Durand, L.: Dussurget, O.: Entian, K.D.: Fsihi
D.: Jones, L.M.: Karst, U.
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A:Cross-references: GB:BA000019: PIDN:BAB72663.1; PID:g17130051; GSPDB:GN00179
A:Experimental source: strain PCC 7120
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                                                                                       209 PGGRLF1GDAHACQGDGE1CGTAVEFASITTIKVDLJKNWQLSWPRMENAENIMSIGSAR 268
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A;Molecule type: DNA
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Matches 91;
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hypothetical protein TW0119 - Thermotoga maritims (strain MSB8)
C; Pecies: Thermotoga maritims (517516)
C; Pecies: Thermotoga maritims (527616)
C; Pecies: The Colayton R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.B.; Bickey Garrett, M.W.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C, M.
Nature 199, 123-129, 1999
A; Title: Fvidence for lateral gene transfer between Archaea and Bacteria from genome seq.
A; Accession: G7244
A; Status: preliminary
A; Accession: G7244
A; Status: preliminary
A; Accession: G7244
A; Status: Deliminary
A; Cross-references: GB: ARN
A; Residues: 1-285 cARN
A; Residues: 1-285 cARN
A; Cross-references: GB: ARN
A; Cross-references: GB: ARN
A; Gene: TW0119
submitted to the EMBL Data Library, July 1999
Alpescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struck feference cumber: A75001
Alkeference cumber: A75001
Alkession: E75139
Alstatus: preliminary
Almolecule type: DNA
Alkesidues: 1-298 < KAW>
Alkesidues: 1-298 < K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 YTIGPYSTPVLTIEPGDRIIVDTRDAFEGAINSEQDIPSQLLKMPF--LNPQHGPIMVNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                             17.4%; Score 304.5; DB 2; 36.7%; Pred. No. 9.7e-18; iive 45; Mismatches 126;
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Matches 94; Conservative
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Best Local Similarity
Matches 85; Conserv
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probable formamidase (BC 3.5.1.49) F19F18.40 - Arabidopsis thaliana cispecies: Arabidopsis thaliana (mouse-ear cress) c.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999 CACCOSSION: T04712 E.Bevan. M.: Rose, M.: Hempel, S.: Entian, K.D.; Bancroft, I.; Mewes, H.W.: Mayer, submitted to the Protein Sequence Database, March 1999 A:Accussion: T04712 A:Accussion: T0
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                                                                           -VSPEIDSINSL: - - - PUNHGGNMDVPDIGPGSITYPLVRAPGGRLFIGDAHACQGDGE
                                                                                                                                                204 KESATVASEGARTIFGRPEN-GGNCDIKNLSRGSKVFLPVHVPGAKLSIGDLHFSOGDGE
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                                  Alauthors: Kreft, J.; Kuhn, M.; Konst, F.; Karapkat, G.; Naduenc, E.; Maltourdan, A.; Maland, A.; Malands: Kreft, J.; Kuhn, M.; Konst, F.; Karapkat, G.; Naduenc, E.; Maltourdan, A.; Maland, C.; Schluctor, T.; Simoes, N.; Tierrez, A.; Varquex-Scland, J.A.; Voss, H.; Mehland, A.; Milière Comparative genomics of Liszeria species.

A.Reference number: AB1776
A.Reference number: AB1776
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A.Resion: AB1776
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A.Residues: L-299 cGLA>
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A:Experimental source: strain 972h-; cosmid c869
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C;Species: Schizosaccharomyces pombe
C;Species: 33-Dcc-1999 #scquence_revision 03-Dcc-1999 #text_change 03-Dcc-1999
C;Accession: T39115
R;Hunt, C; Aves, S; McDougall, R.C.; Rajaudream, M.A.; Barrell, B.G.
S;Emint, C; Aves, S; McDougall, R.C.; Rajaudream, M.A.; Barrell, B.G.
S;Emint, C; Aves, S; McDougall, R.C.; Rajaudream, M.A.; Barrell, B.G.
S;Emint, C; Aves, S; McDougall, R.C.; Rajaudream, M.A.; Barrell, B.G.
S;Entus: preliminary; translated from GB/EMBL/DDHJ
A;Residues; 1-410 <HUN>
A;Residues; 1-410 <HUN>
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Best Local Similarity 26.1%
Matches 92; Conservative
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849-852, 2001
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Best Local Similarity
Matches 79; Conserv
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A.Gene: SPDB:SPAC869.04
A.Map position: 1
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1 1 1 1 1 1 1 1 1 1	139 131 RESULT 13 RESULT 13 F71097 174 Mypothetical protein PH1641 - Pyrococcus horikoshii C; Eate: 14-Aug-1998 #sequence_revision 14-Aug-1998 # C; Accession: F71097 Rewarabaysal, Y.; Sawada, M.; Horikawa, H.; Haikaw X.; Ohfuku, Y.; Tanahashi, T.; Tanaka, T.; Kudoh, Y DNA Res. 5, 55-76, 1998 A.Title: Complete sequence and gene organization of A.Title: Complete: A71000, MulD:98344137; PMID:9679 A.Status: Preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Status: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Status: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Status: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Status: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Status: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Status: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Status: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Status: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Status: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Status: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Moloculo type: DM: A.Status: preliminary: preliminary: preliminary: nucleic acid sequence not sho A.Moloculo type: DM: A.Moloculo type	University Uni
A; Residues: 1-432 cBEV> A; Cross-references: EMBL:AL035605 A; Experimental source: cultivar columbia; BAC clone F19F18 C; Genetics: A; Map position: 4 A; Introns: 73/3; 153/1; 196/3; 275/2; 356/3; 392/3 A; Note: F19F18.40 C; Keywords: hydrolase Query Match Rest Local Similarity 24.1%; Pred. No. 1.6e-09; Matches 92; Conservative 44; Mismatches 140; indels 106; Gaps Qy 28 EMQKEFHYILOPYSTPULTEPGDRITUDTROMEGAI:NSEODIPSQLIKMFFINPO Db 20 QODQPLHNRWHEDIPPAEVMAGEFRVEWIDAMGGVIKUDSASSIKNLVITITHHIL	I I I I I I I I I I	PESCLT 12 S74213 formamidase (EC 3.5.1.49) A · Mc:hylophilus methylotrophus C;Species: McUhylophilus methylotrophus C;Species: McDec1997 *Esquence_revision 12-Dec-1997 *text_change 20.0un-2000 C;Accession: S74213: \$78115 R;Wyborn, N.R.; Millis, J. Williams, S.G.; Jones, C.W. R;Wyborn, N.R.; Millis, J. Williams, S.G.; Jones, C.W. Eur. J. Biochem. 240, 314-322, 1996 A;Title: Molecular characterisation of formamidase from Methylophilis methyls A;Reference number: S74213; WUD:96439058; PMID:8841393 A;Residues: 1-407 <wyb> A;Residues: 1-407 <wyb> A;Residues: 1-407 <wyb> A;Roossreferences: EMBL:X99632; NID:q1480104; PIDN:CAA67953.1; PID:q14861105 A;Rootule Lype: Drottein A;Residues: 1-5;44-47;172-176;211-215 <wyc> C;Genetics: A;Gene: findA C;Reywords: hydrolase Cuery Match Best Local Similarity 25:58; Pred, No. 3e-09; Matches 84; Conservative 38; Mismatches 116; Indels 91; Gaps A; Collentics: A;Gene: findA C;Reywords: hydrolase C;Reywords: hydrolase C;Reywords: Mismatches 116; Indels 91; Gaps A; Collentics: A; Conservative 38; Mismatches 116; Indels 91; Gaps A; Collentics: A; Collentics A; A;</wyc></wyb></wyb></wyb>

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                                           C.Species: Mycobacterium smeqmatis
C.Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_crange 22-Not:-1999
C.Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_crange 22-Not:-1999
C.Accession: A47696
R.Mahenthiralingam, E.: Diaper, P.; Davis, E.O.; Colston, M.C.
J. Gen. Microbiol. 139, 575-583, 1993
A.Title: Cloning and sequencing of the gene which encodes the highly inducible acetation and reference number: A47696
A.Steference number: A47696
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A.Stevesion: A7775; GB:S59037; NID:q3:12080; PIDN:CAA40462.i: PID::q3:12081
A.Cross-references: GB:X57775; GB:S59037; NID:q3:12080; PIDN:CAA40462.i: PID::q3:12081
A.Note: sequence inconsistent with the nucleotide translation:
A.Note: sequence extracted from NCBI backbone (NCBIN:129965, NCBIP:12976)
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A:Note: F19F18.50
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Compagen Ltd.
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GenCore version
Copyright (c) 1993 - 2003
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JVRA_NETGO
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    protein search, using sw model

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMHL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Bacteria: Proteobacteria: beta subdivision; Methylophilus group;
Methylophilus.
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P53463 h
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C86090 s
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P92176 l
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SIRAIN-AS1 / ATCC 53528 / DSM 46235 / NCIB 16315;
MEDLINE-96439058; Pubmed-684193;
WEDLINE-96439058; N. MILLS J., WILLIAMS S.G., Jones G.W.;
"Molecular characterisation of formamidase from Methylophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 204.5; DB 1; Length 407; 25.5%; Pred. No. 1.9e-09; ive 38; Mismatches 116; Indels 91;
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SUBDNIT: HOMOTRIMER.
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15-JUN-2002 (Rel. 41, Last annotation update)
Formamidase (EC 3.5.1.49) (Formamide amidohydrolase).
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TYCC_BACBR
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MT30 YERNSA
MT30 YERST
ACTM_HELER
TIVB_MYCLE
TIVB_MYCLE
PPK_SALTI
PPK_SALT
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Pfam; PF03069; Fmda_Amda; 1.
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq.
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   methylotrophus.
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                                                                                                                                       § SRHVPGVRYTGITHPGLFGTAPSPDLJAKWNE -- RERALIATDPDRV -- - - PPLALPP 196
                                                                                                                                                                                                                                                                                                                                                                                     85 DULIVDIEDIGPVPQTNGPNCGEGWGYSGLFAKVNGGGFETDYYPDAYKAIWDFHGQOCT 144
                                                                     ------GITGI----DLTAMINDPLPEKVRMIKIDSEKVYWSKRHTLPYKP 165
                                                                                                                                                                                                            166 HI-GTL--SVSPE1----DSINSLTPDNHGGNMDVPDIGPGS-ITYPLVRAPGGRLFI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 GDAHACQGDGE1--CGTAVEFASTTTIKVDLIKNWOLSWPRMENAENIMSIGSARPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteobactería; beta subdivision; Neisseríaceae; Neisseria.
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SEQUENCE 97340932. PubMed-9157406;

Black C.G., Fyfe J.A.M., Davies J.K.;

"Cloning, nucleotide sequence and transcriptional analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Literpro: IPROG4602; Uvrā.
Pfam: PF00005; ABC_tran: 2.
Profbum: PD000066: ABC_transportr; 1.
TIGRAMS: TIGRA066: ABC_transportr; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
SOS_response; Excision nuclease; DNA repair: AIP-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------DEGENTRIAYRDLIYWLVE---DEGEGWDAYMLL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 WLTFIGISVDHAENRNAYMDAT-MAYRNACLNAIEYLKKWGYTGEQAYLIL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%: Score 99.5; UB 1; Length 950:
20.6%; Pred. No. 2.4;
Lve 56; Mismatches 127; Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359806240AADD6F; CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51-NOV-1997 (Rel. 35, Created)
51-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIP (POTENTIAL).
AIP (POTENTIAL).
C4-TYPE.
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LiterPro; IPR064602; Uvra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria gonorrhoeae.
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Matches 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVRA_NEISC
QSC968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZN_FING
ZN_FING
SEQTENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chery Match
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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                                                                                                                        ---SGPIGVEGAEPGDLWVVVLLDVGTPDDSOWG----FNGLFAKENGGGFLJCHFP 122
                                                                                                                                                                                                                                                     242 KDGGLSMGDEHFSQGDGETTFCG-ATEMAGYEDTKVGDIK-------DGVKKYGT 284
                                                                 82 NPONGPIMVNGAEKGDVLAVYIBSMLPRGVDPYGJCAMIPHFGGJJGTDL-JAMLNDPLP (40
                                                                                                                                                                                                         ----IDSINSITPONHGGNMDVPDIGPGSITYPLVRA 208
                                                                                                                                                                                                                                                                                                                                                                                                                  182 VPPLACPPTSGSAVMGRLSGDAAKKAAAEGARTVPPHDHGGNGDJKNLJKGSRVYFFVVV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ų:
Ch
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EQDGQIHNRWHPDLPMIAMVKPGDEFRVECMDWTGGQIGNNDSANDVRDV--DLTGVHYL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gen. Microbiol, 139:575-583(1993).
- FUNCTION: ALLOWS ACETAMIDS TO BE USED AS A SOLE CARHON OR NITROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 PGGKLFIGDAHACQGDGEI -CGTAVEFASITTIKVDLIKNWQLSWPAMENABNIMSIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 TIEPGDRIIVDTRDAFEGAL----NSEQDI---PSGLLKMPPLNPQNGP1MVNGAEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridac; Actinomycetales; Corynebacterinoae; Mycobacteriaceae; Mycobacterium; NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 178.5; DB 1; Length 465;
Pred. No. 2.6e-67;
9; Mismatches 103; Indels 117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 1-23; 81-100 AND 180-194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mahenthiralingam E., Draper P., Davis E.O., Colston M.J.: "Cloning and Sequencing of the gene which encodes the highly inducible acetamidase of Mycobacterium smegmatis."; J. Gen. Microbiol. 139:575-583(1993).

    -!- CATALYTIC ACTIVITY: Acetamide + H(2)0 - acetate + NH(3).
    -!- SIMILARITY: STRONG, TO M.METHYLOTROPHUS FORMAMIDIASE.

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05E2E359210E0BF2 CRC64;
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15-JUN-2002 (Rel. 41, Last ammotation update)
Acetamidase (EC 3.5.1.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 ARPLEDATRI--AYRDLIYWDAEDFGEEQ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NCIC 8159;
MEDLINE-93232774; PubMed=8473963;
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InterPro; IPRO04304; FmdA_Anda.
Pfam: PF03069; FmdA_Amda: 1.
Hydrolase.
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SEQUENCE 405 AA; 43833 MW;
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26.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium smegmatis.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMDA_MYCSM
Q07838;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMDA_MYCSM AMDA_WA COTOR B TO 10-NOV DT 10-NOV
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20;

Gaps

5 g us-10-086-082-2.rsp

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                                                                                                                                                                                                                                                                                                                                         233
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFFDAVPIVSRKLQT; MOVGLGYIRIGQSATTLSGGEAQRVKLALELSKRJISRTLY11 865
                                                                                                                                                                                                                                                                                          686 GLEHLDKVINVDQSPIGRTPRSNPATYTGLFTPIRELFAGVPISRERGYNVGRESFNVKG 745
                                                                                                                      597 TGQYLGGKKSIAVPSERIP-VNP-GRMLVLKGARGNNLKNVTLE--LPLG-----LI 644
                                                                                                                                                                  121 PHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRHTLPYKPHLGTLSVSPEIDSIN 180
                                                                                                                                                                                                                                                     SLTPDNHGGNMDVPD1G-----PGSIT------YPLVRAPG---GRLFI---- 215
                                                                                                                                                                                                                                                                                                                                                                             746 GRCEACQGDGVIKVEMHFLPDVYVPCEVCHGKRYNRETLE1OYKGKNISQVLDMIVEEAR 805
                                          RDLGNSVIVVEHDEDAIREADFVVDMGPGAG-----EHGGNVLI--ADTPENVAKCEKSV 596
                                                                                                                                                                                                        645 TCITGVSGSGKSTLINDT..----AKITARELNRAQEEPAPY--------DDIR 685
  RGVGAGRKPVTHHLTEEMQKEPHYIIGPYSIPVLT1EPGDRIIVDTRDAFEGAINSEODI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rectally the ABC excision nuclease is a DNA repair enzyme that catalyzes the excision reaction of UV-damaged nucleotide segments producing oligomers having the modified base(S). UVA is an ATPase and a DNA-binding protein that preferentially binds single-stranded or UV-irradiated double-stranded DNA (By similarity).
-!- SUBMUII: Consists of three subunits; uvra, uvrB and uvrC.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
(n)
                                                                                                                                                                                                                                                                                                                                       ----GTAVB---
                                                                                    PSQLI,------KMPFUNPQNGPIMVNGAEKGDVLAVYIESMLPRGVDPYGICAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JVRA OR MMA1159.
Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhil J., Achtman M., James K.D., Rentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Bavies R.M., Davies R.M., Davies R., Monie S., Mongali K., Chail M.A., Holrayd Jagels K., Leather S., Monie S., Mongali K., Chail M.A., Holrayd Whitehead S., Spratt B.G., Sarrell B.G., Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 2491.";
Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                       --FASITTI--KVDLIKNWQLSWPRMENAENIMSIGSARPLEDATRIAYRD-
                                                                                                                                                                                                                                                                                                                                     216 GDAHACQGDG--------EIC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rej. 41, Created)
15-JUN-2002 (Rel. 41, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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MEDLINE-20222556; PubMed-10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-DEGFEQWDAYMLLSQCGKVR-LGNMV 312
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09JJS4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRHTLPYKPHIGTLSVSPEIDSIN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               545 TC1TGVSGSGKSTLINDTL----AKIIARELNRAQEEPAPY------DDIR 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                686 GLEHLDKVINVDQSPIGRTPRSNPATYTGLFTPIRELFASVPLSRERGYNVGRESFNVKG 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 PSQLL------KMPFLNPQNGPIMVNGAEKGDVI,AVYIESMI,PRGVDPYGICAMI 120
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"Molecular and blochemical characterization of the recombinant amidase
from "yperthermophilic archaeon Sulfolobus solfataricus.";
Extremophiles 5:183-192(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRCEACQGDGVIKVEMHFLPDVYVPCEVCHGKRYNRETLEIQYKGKNISQVLDMTVEEAC
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                                                         Pfam; PF00005; ABC_Lran; 2.
Proton; PD00006; ABC_transportr: 1.
TIGRPAMs; TIGRO0630; uvra; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat; DNA-binding; Zinc-finger; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125;
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STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-97055432; PubMed-8899719;
Seasen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 948;
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                                                                                                                                                                                                                                                    42 49 ÅTP (PÖTENTIAL).
649 656 ATP (POTENTIAL).
262 289 C4-TYPE.
748 774 C4-TYPE.
946 AA; 105191 MM; E98717DF762B9A0D CRC64;
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61-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
8502122 OR C02016 OR C62_017.
                                                                                                                                                                                                                                                                                                                                                                                                                                               .6%; Score 98.5; Dl
.6%; Pred. No. 2.9;
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STRAIN*ATCC 49255 / DSM 5833 / MT-4;
MEDLINE=21346015; PubMed=11453462;
InterPro; iPR003439; ABC_transportr.
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                                 IPR0C4602; UvrA.
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ZN_FING
SEQUENCE
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NP_BIND
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AMID_SULSO
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                                                                                                                                                                                                         STRAINFATCH 35092 / DSM 1617 / P2;

MEDLINE-2132296; PubMed-11427726;

MEDLINE-2133296; PubMed-11427726;

A Mayez M.J. Chan Welher C.C. Y., Clausen T.G., Curtis B.A.,

A Mayez M.J., Chan Welher C.C. Y., Clausen T.G., Curtis B.A.,

A Mayez M.J., Chan Welher C.C. Y., Clausen T.G., Curtis B.A.,

A Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Pena X.,

A Thi-Nayor H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Carfiebois R.L., Doolittle W.F., Duguet M., Gasterland T.,

A Garrett R.A., Ragan M.A., Sensen C.W., Van der Ocst. J.,

The complete genome of the crearchaece: Suilobbus solfatarious P2.",

Proc. Natl. Acad. Sci. U.S. A. 987835-78472001;

Proc. Natl. Acad. Sci. U.S. A. 987835-78472001;

- - - FUNCTION: Enantioselective, active on 2-to 6-carbon aliphatic

- - - CATALIZIC ACITUTY: A monocarboxylic acid amide + H(2)9 - a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afreement (See http://www.isb-sib.ch/announce/or sond an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 GNMDVPDIGPGSITYPLVRAPGGRLFIGDAHACOGDGFICGTAVEFASITIIKVULIKNW 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBGNIT: Monomer.
-1- MISCELLANEOUS: Active over the pH range 4-9 and at temperatures from 60 degrees to 95 degrees Celsuis.
                         Doclittie W.F., Ragan M.A., Charlebois R.C.,
"Organizational characteristics and information content of an
archdeal genome: 156 kb of sequence from Sulfolobus solfatatious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.6%; Score 97.5; DB 1; Length 504; 21.4%; Pred. No. 1.5;
O.Y., Ponny S.L., Young F., Schenk M.E., Gaasterland T.,
little W.E., Ragan M.A., Charlebois R.L.,
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SEQUENCE 504 AA: 55655 MW; A9103AB7D09AB8EE CRC64;
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                                                                                                                                     Mol. Microbiol. 22:175-191(1996).
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Pfam; PF01425; Amidase; 1.
PROSITE; PS00571; AMIDASES; 1.
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EMBL; AE006819; AAK42301.1;
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                                                                                                                                                                                        SEQUENCE FROM N.A.
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949 AA

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STANDARD:

JVRA_NEIMB

UVRA_NEIMB ID UVRA_N

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Tettein H., Saunders N.J., Heidelberg J., Joffries A.C., Nelson K.E., S. Tettein H., Saunders N.J., Heidelberg J., Joffries A.C., Nelson K.E., Eiser J.A., Retchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Andron H., Cacko A., Parkscy D.S., Biair E., Cittore H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Oin H., Vanathevan J., Cotton M.D., Utterback T.R., Khouri H., Oin H., Vanathevan J., Complete genome sequence of Neisseria meningitidis serogroup B strain R. Tomplete genome sequence of Neisseria meningitidis serogroup B strain R. Schone 287:1809-1815(2003).

R. Schone 287:1809-1815(2003).

R. Schone 287:1809-1815(2003).

R. Schone 287:1809-1815(2003).

Catalyzes the excision reaction of UV-damaged nucleotide segments producing oligomers having the modified base(S). Uvra is an Arpase producing oligomers having the modified base(S). Uvra is an Arpase cand a DNA-binding protein that preferentially binds single-stranded or UV-iradiated double-stranded DNA (By similarity).

C. SCHOLT: Consists of three subunits: uvra, uvrB and uvrc.

SCHOLT: Consists of three subunits: uvra, uvrB and uvrc.

C. SCHOLT: Consists of three subunits: uvra, uvrB and uvrc.

C. SCHOLT: SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by inon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645 TCITGVSGSGKSTLINDTL----AKITARELNRAQEEPAPF------DDIH 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGVGAGRKPVTHHLTEEMQKEFHYT1GPYSTPVLT1EPGDR1IVDTRDAFEGAINSEQDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544 RDLGNSVIVVEHDEDAIREADFVVDMGPGAG----EHGGNVLI--ADTPENVAQCENSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 PSQLL------KMPFLNPQNGPIMVNGAEKGDVJAVYIESMLPRGVCPYGICAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Mismatches 127; Indels 125; Gaps
                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, beta subdivision, Neisseriaceae, Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; ...
LitterPro; Pro04602; vv....
LitterPro; PR004602; vv....
Pfam: PP00006; ABC_tran; 2.
Probom; PD00006; ABC_transportr; 1.
TIGRAMS; TIGROGO30; uvra; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat; DNA-binding; Zinc-finger; Complete protecome.

20A-binding; Zinc-finger; Complete Protecome.
42 49 ATP (POTENTIAL).
656 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             748 774 C4-TYPE.
949 AA; 105536 MW; 153F5AE2D48CDD35 CRC64;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last unnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.6%; Score 97.5; Di
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Literpro; IPR004602; UvrA.
                                                                                                                                                                                                           Neisseria meningitidis (serogroup B)
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MC58 / Serogroup B;
MEDLINE-20175755; PubMed-10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE0C2447; AAF41368.1; -.
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                                                                                                                         Excinuclease ABC subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.6%
Cuery Match
Best Local Similarity 20.4%
Matches 79: Conservative
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                    UVRA OR NMB0962
                                                                                                                                                                                                                                                                                         NCBI_TaxID-491;
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01-JUN-1994 (Rel. 25, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Nitrate reductase (NADPH) (EC 1.6.6.3) (NR).
                                                                                                                                                                                                                                                                                                              867 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001199; Cyt_B5.
InterPro; IPR001834; Cyt_B5_reductase.
InterPro; IPR000572; Buk_Mb_oxred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001433: Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: M77022; -; NOT_ANNOTATED_CDS.
PIR: JQ1525; JQ1525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piam; PF00173; heme_1; 1. Pfam; PF00174; oxidored_molyb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00175; NAD_binding; 1.
Pfam; PF00970; FAD_binding_6; 1.
Pfam; PF03404; Mo-co_dimer; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005066; Mo-co_dimer
  GGNMDVPDIGPGS1-----
                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2CND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P17571;
                                                                                                                                                                                                                                                                                                           NIA_ASPNG
P36858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro:
                                                                                                                                                                                                                                                                  RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 PEKDPKEIEKAKK-----INPQ--SGYPKCLLCIENVGFAGN-----LNHPARGN 199
                                       GLEHLINKVINVDOSPIGRIPRSNPATYTGLFTDIRELFAGVPLSRERGYNVGRESFKVKG 745
                                                                                                                                                                234 --FASITTI--KVDLIKNWQLSWPPMENABNIMSIGSARPLEDATRIAYRD---LIYWLV 286
                                                                                                                                                                                                     EFFDAVPIVSRKLOILMDVGLGYIRLGOSATILSGGEAQRVKLALELSKRDIGRILYILD 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 VRMIKLD-----SEKVYWSKRHTLPYKPHIGTLSVSPE----IDSINSLTPDNH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 LRIIPVKVAGEQWYFQYSPYVYYNEHCILLHEEHI-PMKISEKTFVRLFDFIDQFPHYFM 258
                                                                                  ----- GTAVE--- 233
                                                                                                                       GRCEACQGDGVIKVEMHFLPDVYVPCEVCHGKRYNRETLETQYKGKNISGVLDMTVHEAR 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 PONGPIMVNGAEKGDVLAVYIESMLPRGVDPYGICAMIPHFGSLIGTDLTAMLNDPLPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
SLIPDNEGGNMDVPDIG----PGSIT-----YPLVRAPG---GRLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10) (Gal-1-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SERVARMA / JCM 11007;
MEDITNE-2199216; PubMed-11997336;
MEDITNE-2199216; PubMed-11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling in the Y., Wang J., Yu J., Yang H.;
Tan H., Chen R., Wang J., Yu J., Yang H.;
A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-730(2002).
-! CATALYTIC ACTIVITY: UTP + alpha-D-galactose I-phospirate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.4%; Score 94.5; DB 1; Length 519; 20.2%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS91163: GAL_P_UDE_TRANSF_II; FALSE_NEG.
Transferase; Nucleoti3yltransferase; Salactose metabolism;
Complete proteome.
SEQUENCE 519 AA; 60467 MW; OBF788A4EA08ED75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoanaerobacter tengcongensis.
Bacteria: Firmleutes; Clostridia: Thermoanaerobacteriales;
Thermoanaerobacteriaceac; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: Galactose metabolism; second step.
SUBCELULAR LOCATION: Cytoplasmin (Potential).
SIMILARITY: BELONGS TO THE GALACTUSE-1-PHOSPHATE
URIDYLYLTRANSFERASE FAMILY 2.
                                                                                GDAHACQGDG-------EIC------
                                                                                                                                                                                                                                                                                                                                                                                            519 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Mismatches
                                                                                                                                                                                                                                               287 E-DFGFEQWDAYMLI,SQCGKVR-LGNMV 312
                                                                                                                                                                                                                                                                                      866 EPTTGLHFADIALLLEVIGRLKGKGNSI 893
                                                                                                                                                                                                                                                                                                                                                                                            PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diphosphate - UDP-galactose.
                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel, 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AEC13143; AAM25108.1; -
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                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uridylyltransferase).
GALT OR TTE1929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-119072
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002
15-JUN-2002
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Best Local S
Matches 56
                                                                                516
                                                                                                                       746
                                                                                                                                                                                                                                                                                                                                                                                          GALT_THI
QBR8R6;
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---IYPLVRAPGGRLF1GDAHACQGDGEICGTAVEFAS 236
                                                                                                                       301 - KEVKAGILK-WPMSVIRI,-----SSKDREKLTKLSSH1LNVW--KGYSDESVDV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-92175518: PubMcd=1541396;
Jakles S.E., Campbell E.L., Punt P.J., Hawker K.L., Contreras R.,
Takkins A.R., van den Hondel C.A.M.J.J., Kinghorn J.R.;
"Te Aspergillus niger niabl gene encoding nitrate reductase: upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST STEP OF NITRATE ASSIMILATION IN PLANTS, FUNCT AND BACTERIA.

CATALYTIC ACTUVITY: NADPH + nitrate - NADP(+) + nitrite + H(2)O.

COPACION: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)

AND ONE MOLYBERNUM ATON.

SUBGUIT: HOMODIMER (BY SIMILARITY).
                                                                                  237 ITTIKVDLIKNWOLSWPRMENAENIMSIGSARPLEDATRIAYRDLIYWLVEDFGFFQWDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY, HEME-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukarýsta, Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic frichocomaceae; Aspergillus.
NCBL_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER (BY SIMILARITY).
SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-TERMINAL DOMAIN.
SIMI.ARITY: CONTAINS 1 CYTOCHROME B5 FAMILY, HEME-BINDING DO SIMI.ARITY: CONTAINS 1 CYTOCHROME REDUCTASES IN THE C-TERMINAL DOMAIN.
                                    259 GSNADIPIVG-GSILVHEHFQGGRHTFPMEEAPIEEYFIHPKY-----
                                                                                                                                                                297 YMLLSQCGKVRLGNMVDP-----KYTVGAMLNKN 325
                                                                                                                                                                                                    347 LAYSEKDGKIVPHNTITPIARFNKEGEYEIDLVLRNN 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide and amino acid sequence comparisons.
Gene [11]:149-155(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0406; CYTBSRDTASE.
PRINTS; PRO0363; CYTOCHROMEB5.
PRINTS; PRO0407; EUMOPTERIN.
PRODSITE; PS00121; CYLLS; 1.
PROSITE; PS00121; CYTOCHROME_B5_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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There are no restrictions on

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European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDITURE-22011499: Pubmed-1717443;
Kikuta Y., Sogawa K., Haniu M., Kinosaki M., Kusunose E., Nojimu Y.,
Kikuta Y., Sogawa K., Haniu M., Kinosaki M., Kusunose E., Nojimu Y.,
Tamanoto S., Ichihara K., Kusunose M., Puji: Kuriyama Y.,
"A nove! species of cytochrore P-450 (P-4501b) specific for the small
intestine of rabbits. cDNA cioning and its expression in DCS ceils.",
J. Blol. Chem. 266:17821-17825(1991).
-:- FUNCTION: CATALYZES THE N-DEMEIHYLATION OF BENZPHETAMINE TO
                                                                                                                                                                                                                                                                                                                                                                                              88 IMVNGAEKGDVLAVY1ESMLPRGVDPYG1C----AMIPHFG-----GLIGIDL/TAMLND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 PLPEKVRMIKLDSEKVYWSKRHTL2-----YKPH;GTLSVSPEIDS:----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 PL-RAVVPGQIGGRSVKWLKKLILIDAPSDNWYHIYDNRVLPINVSPEMSSSDPNWWRDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----NSLTPONHGGNMDVPDIGPGSTfYPLVRAPGGRLFIGDAHACGGEGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 TRVE-----ISLDKGKSWRLANISYAEDKYRDFEGDLFGGRVHMSWRETCFCWCFWSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                          202 VCMEGADK------LPNGY--YGTSIKINWAMDPNRGIMLNHKMNGEDLAFUHGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 RYAIYDLNVNSSVVYPEHKEVLDLASAGPSYNVKGYAYAGGGRRT-------
                                                                                                                                                                                                                                                                                                                              ilarity 20.7%; Pred. No. 6;
Conservative 29; Mismatches 95; indeis 118; Gaps
                                                                                                                                     HEME-BINDING (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
FLAVIN-BINDING COMMIN (BY SIMILARITY).
NADP (BY SYMILARITY).
NADP (BY SYMILARITY).
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Eukaryota, Metazoa: Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Laqomofpha, Leporidae, Cryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- CATALYTIC ACTIVITY: RH - reduced flavoprotein + 5(2) ~ ROH oxidized flavoprotein + H(2)0.
-: SUBCELLULAR LOCATION: Membrane-bound, Endoplasmic reticulum.
-: TISSUE SPECIFICITY: SMALD TIBESTONE.
-:- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                        MOLYBDENUM-PTERIN (POTENTIAL).
                                                                     MOLYBDENUM-PTERIN (POTENTIAL).
                      ductase: Flavoprotein; FAD; NADP; Heme; Moiybdenum; assimilation.
                                                                                                                                                                                                                                                                                                     5.4%; Score 94; DB 1; Length 867; 20,7%; Pred, No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last ennotation update)
Cytochrome P450 231 (EC 1:14.14.1) (CYPIIJ1) (P-4501B).
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    MOLYBDOFTERIN_EUK;
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                                                                                                                                                                                                                                                           97188 MW:
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203
399
549
572
867
846
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518
549
612
837
867 AA:
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,65500Sq
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                        Oxidoreductase:
Nitrate assimila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9986;
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Best Local Simi
Matches 63;
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P52786;
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BINDING
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NP_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKEQRRFALMTLRNFGLGKKSLEERIQEEARHLTEAMEKEGGQPFDAHFKINNAVSNIIC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 LELEVSRMLENHKKDWNPAETRDFIDAYLKEMSKYPGSATSSFNEENLICSTLDLF--LA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 FASITTIKVD-LIKNWQLSWPRMENAENIMSIGSARPLEDATRIAYRDLIYW---LVEDF 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 SITFGERFEYHDGOFQELEKLFDEVMYLEASMLCQLYNIFPWIMKFLPGAHQTLFSNWKK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTDLTA------MINDPLPEKVRMIKLDSEKVYW----SKRHTLPYKPH1GTI.SVS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 GTETTSDMRWGLLFMALYPEIQEKVH-AEIDSVIGQWQQPSMASRESLPY----INAVI 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 PEIDSINSLTPDNHGGNMDVPDIGPGSITYPLVRAPGGRLFIGDAHACQGDGEICGTAVE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 WLEE---SIMAKRGVGAGRKPV-----THHLTEEMQKE-----FHYTI-GPYSTPVL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 IIEPGDRI-----IVDTRDAFEGAINSEQDIPSQLLK-----MPF1,-----NPQN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 GPIMV-----DPYGICAMIPHFGGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97237725; PubMed-9084180:
Sa-Nogucira I.M.G., Nogueira T.V., Soares S., de Lencastre H.;
"The Bacillus subtilis L-arabinose (ara) operon: nucleotide sequence,
genetic organization and expression.";
Microbiology 143:957-969(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                   PROSITE: PS06086, CYTOCHROME_P450; 1.
Oxidoreductase: Monooxygenase; Electrou transport; Membrane; Heme;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1: Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Firmicutes, Baciliales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                           446 446 HEME (BY SIMILARITY).
500 AA; 57194 MW; AQEEE628E5FF23DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. Nc. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.3%; Score 92; 22.3%; Pred. Nc.
                                                                                                                                                                                                                            InterPro: IPR001128; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                    Microsome, Endoplasmic reticulum.
INIT_MET 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                        A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Kunst F., Ogasawara N., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Bolotin A., Borchert S.,

RA Borriss R., Boursier C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Canberton I.F., Cummings N.J., Daniel R.A.,

RA Brouillet S.D., Errington J., Concerton I.F., Cummings N.J., Daniel R.A.,

RA Derizot F., Deviner K.M., Dusterhoft A., Ehrlich S.D., Mamerson P.T.,

RA Dinns J.Y., Claser P., Coffeen A., Galightly E.J., Grandi G.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Guiseppi G. Guy B.J., Haga K., Halech J., Brawood C.R., Henaut A.,

RA Mosser P., Coffeen A., Golightly E.J., Laya M., Jones L.,

RA Acaramata D., Kasahara Y., Klaerr E., Itaya M., Jones L.,

RA Kutta K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kutta K., Lapidus A., Lardinois S., Lauber J., Bararevic V.,

RA Kutta K., Lapidus A., Lardinois S., Lauber J., Bararevic V.,

RA Medina N., Mellado R.P., Mizuno M., Mossti D., Nakai S., Noback M.,

RA Presecan E., Pujic P., Purnolle B., Roche B., Rose M., Sadaie Y.,

RA Scanlan E., Schleich S., Schroeter R., Scolfone F.,

Scholar B., Schleich S., Schroeter R., Scolfone F.,

Scholar A., Scanlan E., Schleich S., Schroeter R., Schleich S.,

RA Schigubi J., Sekowska A., Schroeter R., Schroeter R., Schleich S.,

RA Tosato V., Uchiyama S., Vandenbel M., Vannier F., Vatsarotti A.,

RA Tosato V., Wedler E., Wedler F., Wedler F., Weller F., Vatsarotti A.,

RA Tosato V., Weller R., Wedler F., Welmer F., Vatsarotti A.,

RA Viari A., Yashiawa H.F., Zumstein E., Yoshikawa H., Saccilus S.,

RA Subrils R.,

Ra Schiller E., Weller C., Roche E., Roching R., Yashikawa H.,

Ra Schiller E., Weller E., Weller E., Weller P., Weller E.,

Ra Schiller E., Weller E., Weller E., Weller P., Weller E., Weller E., Weller P., Weller E., Weller E., Weller P., Weller E., Weller P., Weller E., Weller P., Weller E., Roche E., Personi R.,

Ra Schiller E., Schiller E., Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dota i.d., Tavares P., Sa-Noqueira 1.M.G.;
Mode of action of AraR, the key regulator of L-arabicose metabolism
in Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 33:475-489(1999).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha Larabinosides.
-i- INDUCTION: Transcription is repressed by qlucose and by the binding of araR to the Operon promoter. Larabinose acts as an inducer by inhibiting the binding of araR to the Shadan
                                              Wipat A., Carter N., Brignell C.S., Guy J.S., Piper K., Sanders J., Emmerson P.T., Harwood C.R., "The dnaB-pheA (256 degrees-240 degrees) region of the Bacilius subtlins chromosome containing genes responsible for stress responses the utilization of plant cell walls and primary metabolism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allowing expression of the gene. SIMILARITY: BELONGS TO FAMILY 51 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: X89810; CAA61937.1; -.
EMBL: 275208; CAA99595.1; -.
EMBL: 299118; CAB14832.1; -.
Subtlinist; BG11900; abfA.
Hydrotiase; Glycosidase; Complete proteome.
CONFLICT 114 114 P -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                             MEDLINE=98044033; PubMed-9384377;
                        MEDLINE-97124191; PubMed-8969504;
                                                                                                                                                                                                   Microbiology 142:3067-3078(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1397).
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                       STRAIN=168
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hetween the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                             54 VQSL-IKELQVPIIRYPGGN-FI.SGYMWELGVGPVENRPRRLDIAWQTTETNEVGTNEFL 111
                                                                                                                               141. EKVRMIKIDSE------KVYWSKRHTLPYKPHIGTLSVSPEIDSINSLTPDNHGGNMD 192
                                                                                                                                                                                                                                                                                                          251 SWPRMENAENIMSIG-SARPLEDATRIAYRDLI-----YW--IVEDFGFEQWDAYM 298
                                                                                                                                                                                                                                                                                                                                                   112 SWPKKVNTEVNMAVNLGTRGID----AARNLVEYCNHPKGSYWSDLRRSHGYEQ--PYG 164
                                                                                                                                                                        2 KKARMI-VDKEYKIGEVDKRIYGS-----FIUHMGR-AVYEGIYEPDHPEADEDGFRKD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whele-genome random sequencing and assembly of Baemophilus influentae
                                                                                                                                                                                                                  .93 VPDIGPGSITYPLVRAPGGRLFIGDAHACQGDGEICG--TAVEFASITTIKVDLIKNWQL
                                                                                   Indels 43; Gaps
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MEDINE-95350630; PubMed=7542800;
Profit NE-95350630; PubMed=7542800;
Reflavage A.R., Bult C.J., Tomb J.-F., Doughorty B.A., Merrick J.M.,
Reflavage A.R., Sulton G., Eltzhugh W., Fields C.A., Godayne J.D.,
McMarchey K., Sulton G., Eltzhugh W., Riddon C.A., Godayne J.D.,
Weidham J.F., Phillips C.A., Springs T., Hedblom E., Cotton M.D.,
Ultorbock T.R., Hanna M.C., Nayvon D.T., Sauddek D.M., Brandon R.C.,
Grohm C.L., McDonald i.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White C., Clayton R.A., Korlavage A.E., Fleischmann R.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: SEEMS IO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                           OB 1; Length 500;
57060 MW; 7397FD52A4987686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- SIMI.ARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        call division protein firsh homolog 1 (EC 3.4.24.-). FTSH-A OR HI335.
                                                                                   74:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last amnotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
-!- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
                                         5.2%; Score 90.5; Distance 5.2%; Score 50.5; Distance 5.7; Social Similarity 25.9%; Pred. No. 5.7; es 52; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                             299 LLSQCGKVRLGNMVDPKYTVG 319
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U32812; AAC22979.1; -. TIGR; HI1335; -.
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500 AA:
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P71377;
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                                              Coery Natch
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MEDLINE-93054553; PubMed-1331061;
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                                                                                                                                                                                                                                                                                                                             STRAIN-K12
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   7 :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 NHGGNMDVPDIGPGSITYPLVRAPGGRLFIGDAHACQGDGEICGTAVEFASITTIKVDLI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304
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                                                                   Pfam: PF00004; AAA; 1.
Pfam: PF01434; Peptidase_M41; 1.
SMART; SM00382; AAA; 1.
TIGRRAMS: IGR01241: FtsH_fam: 1,
PROSITE; PS00674; AAA; 1.
Cell division; AFP-binding; Transmembrane; Hydrolase; Metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | |:: :: | | | : | | EQILKVHMKKVSVAQDVDAMTLARGTP---GYSGADLANLVNEAALFAARVNKRTV;M:E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------PEKVRMIKLDSEK---VYWSKRHTLPYKPHIGTLSVSPEIDS: NSLIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 KNWQLSWPRMENAENIMSIGSARPLEDATRIAYRDLIYWLVEDFGF-EQWDAYMLLSQCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 GVGASR---VRDMFEQAKK-----NAPCL-----IFIDEIDAVGRGRGAGLGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 HDEREQTINGMLVEMDGFSGNDGVIVIAAINRPDVI,DPALTRPGREDRQVVVGLPDVKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------IPRGRALGVIFFLP----EGD-QISISQKQLES----KLSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 YAGRLAEDLIYGEENI-STGASNDIKVATNIARNMYTQW----GFSEKLGPILYTEDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LAVYIESM-LPRGVDPYGICAMIPHFGGLTGTDLTAMLNUPL-------
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01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Polyphosphate kinase (EC. 2.7.4.1) (Polyphosphoric acid kinase) (AIP-
polyphosphate phosphotransferase).
PPK OR B2561 OR Z3764 OR ECS3363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria: Proteobacteria: gamma subdivision: Enterobacteriaceae
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).

LOC (CATANTIC) (BY SIMILARIIY).

BY SIMILARITY.

ZINC (CATALYZIC) (BY SIMILARIIY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 GVGAGKKPVTHHLTEEMQKEFHYTISPYSTFVLTIEPSDRIIVLTRDAF---
                                                                                                                                                                                                                                                                                                                                                                                                                 5.1%; Score 89.5; DB 1; Length 615; 20.4%; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                               70E6DD1E8293839D CRC64;
                                                                                                                                                                                                                           POTENTIAL.
PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 9.4;
53; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 AINSEODIPSOLIKMPFINFQNGPIMVNGAEKGEV----
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                                                                                                                                                                                                                                                                 POTENTIAL.
                   AAA_AIPase_centr.
                             InterPro; IPR003960; AAA_sub.
InterPro; IPR000642; Peptidase_M41.
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                                                                                                                                                                                       Complete proteome.
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635
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                 1PR003959;
                                                                                                                                                                                                                                                                                                                                                                               635 AA;
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les 80; Conser
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                 interPro;
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TRANSMEM
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METAL
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NP_BIND
METAL
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STRAIN-0157:H7 / RIMC 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida I., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiha T., Hattori M., Shinagawa H., Compiete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamagata S., Horluchi T., "Construction of a configuous 874-kb sequence of the Escherichia coli - K12 qenome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features.";
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Kumble K.D., Ahn K., Kornberg A.;
"Phosphohistidyl active sites in polyphosphate kinase of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Mixi T., Mitsuhashi N., Mizobochi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Mizobochi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Tayama T., Oyama S., Saito N., Sampei G., Satch Y., Sivasundaram S., Taqami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamanata S., Horiuchi T.,
                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655.
KEDLINE-97426617; PubMed-9278503;
BEDLINE-FIR. Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Brley M., Collado-Vides J., Glasner J.E., Rode C.K., Mayhew G.F.,
Gregor C., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphoribosylglycinamide transformylase in Escherichia coli K12.";
J. Biol. Chem. 262:10568-10569(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose J.J., Mayhew G.F., Evens P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W. Lim A., Dimalanta E.T., Potamousis K., Apodeca G., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Groome sequence of entrohagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
Akiyama M., Crooke E., Kornberg A.;
"The polyphosphatte kinase gene of Escherichia coli. Isolation and
sequence of the ppk gene and membrane location of the protein.";
J. Biol. Chem. 267:22556-22561(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mau B., Shao Y., "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
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J. Biol. Chem. 268:633-639(1993).
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                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the FNBL custation the European Bioinformatics institute. There are no restrictions on we by non-profit institutions as long as its content is in so way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/assource/creend an email to licensedisb-sib.ch).
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25 LTEEMQKEFHYTIGPYSTPV----LTIEPGD--RIIVDTRDAFEGAINSEQDIPSGI-LK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 ITNEVRRVFNFIENPY-RPVIFDYLMVSPONSRALLYEMVD--REIANAQOGLFSGITLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 ---LN-----NLVDKGLVDRLYAASSSGVPVNLLVRGMCSLIPNLEGISDNIAAISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 MPFLNPQNGPIMVNGAEKGDVLAVYIESM--LPRGVDPYGICAMIPHFGGLTGTDLTAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 NOPLPEKVRMIKLDS---EKVY-----WSKRHTLPYKPHIGTLSVSPET------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERMEDIATE
                                                                                                              SUBCELLULAR LOCATION: Innor membrane-associated,
PTM: An intermediate of this reaction is the autophosphorylated
ppk in which a phosphate is covalently linked to histidine
residues through a NP phond.
SIMILARITY: BELONGS TO THE POLYPHOSPHATE KINASE FAMILY.
SIMILARITY: CONTAINS I PLD PHOSPHODIESTERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                            Ecocone; EG11510; ppk.
InterPro; IPR001736; PLD.
InterPro; IPR003414; PP_kinase.
Pfam: PF00519 PP_Lisse; l.
PR051TE; PS50035; PLD; i.
Transferase: Phosphorylation; Inner membrane; Complete protecume.
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FORMS THE PHOSPHOHISTIDINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGA4_HAEIN STANDARD; PRT; 1849 AA P45386; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.1%; Score 89.5; D:
23.5%; Pred. No. 10;
tive 39; Mismatches
                                                                                                                                                                                                                                                                                                                                     EMBL: M13747, AAA82502.1: ALT_INIT.
EMBL: LOGIS9: -; NOT_ANNOTATED_CDS.
PIR: A24486: A28486.
PIR: A44306; A44306.
                                                                                                                                                                                                                                                                              EMBL: 1.03719: -; NOT_ANNOTATED_CDS.
EMBL: AEC00336: AAC75554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- DSINSTIPDNHGGNMDVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 FSDTVKARYIDKELSNRYVF 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80300 MW:
                                                                                                                                                                                                                                                                                                               EMBL: AF005479; AAG57611.1:
EMBL: AP002561; BAB36786.1:
                                                                                                                                                                                                                                                                                                     D90878; BAA16389.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 23.5 Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.34
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453
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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ID IGA4_HA
AC P45386,
DT 01-NOV
DT 01-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 LILTEKDKQGNLLRRWDVGGDNLELVGNAYTYGIAGTPYKVNHENNGLIGFGNSKEEHSD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 MVNGAEKGDVLAVYJESMLPRGVDPY-----GICAMIPHFGGLTGTDLTAMLNDP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 LPNGIPMIDFSVVDVDKRIATLVNPQYVVGVKHVSNGVSEL--HFGNLNGN-----MNNG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPEKVRMIKLUSEKVYWSKRHTLP--------YKPHIGTLSVSPEI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DAENIMSIGSARPLE---D 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NAKSHRDVSSEENRYYTVEKNNFPTENVISFTTKEEQDAQKRREDYYMPRLDKFVT--EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 DSINSLTPDNHGGNMDVPDIGPGSITYP-LVRAPGGRLFIGDAHACQGDGEICGTAVEFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 APIEASTANNNKGEYNNSD-----KYPAFVRLGSGSQFIYKKGS-----RYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 YALIPYTEAALVRDDVDYQIFRDFAENKGKFSVGATNVEVRDKKNQSL-----GSA
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                              STRAIN=NETT HK61:

PUBLINE-29234949. PubMed=1373717;

PUBLINE-29234949.

"A comparative genetic study of serologically distinct Haemophilus influencase type 1 immunoqlobulin Al proteases.";

"Bacteriol. 174:2913-2921(1992).

-! FUNCTION: VIRULENCE FACTOR: CIEAVES HOST IMMUNOGLOBULIN A PRODUCTNG INTACT FC AND FAB FRAGENIS.

-! CATALYTIC ACTIVITY: Cleavage of immunoqlobulin A molecules at certain Pro-1-Xaa bonds in the hinge region. No small molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Mismatches 128; Indels 136;
                                                                                                                                            Bacteria; Protecbacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR004899; InterPro: IPR004899; Pertact_sup.
Pfam: PF02395; ICA1; 1.
Pfam: PF03212; Pertactin: 2.
Pkinis: PR00921; IGASERPTASE;
Hydro:ase; Serine protease; Iransmembrane; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
IMMUNOGLOBULIN AL PROTEASE.
HELPER PEPTIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE.
W; 79A7D018C7150AEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.0%; Score 88; DB 19.0%; Pred. No. 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202957 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M87491; AAA24968.1; -.
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                                                                                                          Haemophilus influenzae
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1849 AA;
                                                                                                                                                                                                                                                                                    SHOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
:022
                                                                                                                                                                                                              NCB1_TaxID=727;
                                                                                                                                                                                 Haemophilus.
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ACT_SITE
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 YVGDEAQSKRGILTLKYPIEHGIVINWEDMEKIWHHTF--YNE--LRVAPEEHFVLLTHA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 AFEGAINSEQDIPSQLLKMPFLNPQNGPINVNGAEKGDVLAVYIES-----MLPRGVDPY 114
273 ATRIAYRD------GFEQWDAYMLLS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 GICAMIPHFGG------VRMIKLDSE 151
                                                       231 PKGILSODPLINYAVLGDSGSPLFVYDREKGKWLFLGSYDFWAGYNKKSWÇEWNIY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 WLBESIMAKRGVGAGRKPVTHHLT: - - EEMQKEFHYTIGPYSTPVLTTEPGDRTTVDTRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim K., Gooze L., Petersen C., Gut J., Nelson R.G.;
"Isolation, sequence and molecular karyotype analysis of the actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 376;
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; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Alveolata, Apicomplexa, Coccidia: Bimeriida,
Cryptosporidiidae, Cryptosporidium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00268; ACTIN; 1.
PROSITE; PS04406; ACTINS_1; 1.
PROSITE; PS01432; ACTINS_2; 1.
PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
SRUCHURAL protein.
SEQUENCE 376 AA; 42174 MW; 87FF917ACCF46508 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       22, Greated)
22, Last sequence update)
38, Last annotation update)
                                                                                                                                                                                                                                                                                                                     376 AA.
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                                                                                                              302 QCGKVRLGNMVDPKYTVGAMLNKN 325
                                                                                                                                                                  ---KHEFAEKIYQQYSAGSLIGSN 357
                                                                                                                                                                                                                                                                                                                     PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92178278; PubMcd-1542355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; 1PR004001; Actin. InterPro; PR004000; Actin_like. Pfam: PF00022; Actin_like.PRANTS; PR00190; ACTIN.
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HSSP; P02570; 2BTF.
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65; Conservative
                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel.
01-MAY-1992 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5807;
                                                                                                                                                                                                                                                                                                                  ACT_CRYPV
P25183:
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Best Local S
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                     Signature Strington.

Cossins J., Clements J., Catlin G.,
Submitted (JUN-1996) to the EMBL/GenBark/DDBL databases.

Submitted (JUN-1996) to the EMBL/GenBark/DDBL databases.

SIGNIFICAN BAY BE INVOIVED IN TISSUE INJURY AND REMODELING. HAS SIGNIFICANT ELASTOLYTIC ACTIVITY (BY SIMILARITY).

CATALYTIC ACTIVITY: Hydrolysis of soluble and insoluble elastin.

Specific cleavages are also produced at 14-Ala-!-Lou-15 and 16-TI-!-Lou-17 in the B chain of insulin.

CCHACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY (BY SIMILARITY).

SIMILARITY: CONTAINS I HEMOPEXIN-LIKE DOMAIN.
152 KVYWSKRHTLPYKPHIGTLSVSPEIDSINSLTPDNHGGNMDVPDIGPGSITYP-LVRAPG
                                                                                                                                                                                                                                                                                                                                       Ratius norvegious (Rat).
Enkaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Marralia: Eutheria; Rodentia: Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                              065341;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

MACTPHAGE metalloelastase precursor (EC 3.4.24.65) (MME) (Matrix metalloproteinase-12) (MMP-12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase: Metalloprotease; Glycoprotein; Zinc; Zymogen: Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVATION PEPTIDE (BY SIMILARITY). MACROPHAGE METALLOELASTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY CIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYSTEINE SWITCH (BY SIMILARITY)
                                                                    GRLFIGDAHACQGDGE1CGTAVEFASITTIKVDLIKN 247
                                                                                         1:1 :1: | 1 | 1:1 | 267 ----FLG--KEAVGIGE----TTFQSIMKCDLDIRKD 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS0014: HEMOPEXIN: 1. PROSITE: PS00142; ZINC_PROTEASE: 1. PROSITE: PS00546: CYSTEINE_SWITCH: FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEMOPEXIN-LIKE.
                                                                                                                                                                                               465 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: JPR000130; Zn_Wrpeptdse.
Pfam: PF00045; hemopexin: 4.
Pfam: PF00413; Peptidasc_M1C; 1.
Pfam: PF02051; Fragilysin: 1.
PRINTS; PR0138; MATRIXIN.
SMART: SM00120; HX: 4.
                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR001843; Fragilysin.
InterPro; IPR000585; Hemopexin.
InterPro; IPR001818; Matrixin.
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                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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CARBOHYD
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092a16 listeria in O96a16 listeria in O96a10 curospora O84417 pyrocosso C98nv6 rhizobium 1 O91us4 naisseria m O91zpl neisseria m O97zpl neisseria m O97zpl neisseria m O97zpl och O97zpl och O97zpl och O97zpl och O97zpl

096vr2 trichoderma Q9ym2 deinococcus O8xnm Clostildium Q9p853 aspergillus Q9v248 pyrococcus O8tuq7 methanosarc O9etii citrobacter

OByzml anabaena sp Q8r8r6 thermoanaer Q92136 rhizobium m

Q94ap4 arabidopsis Q9szf0 arabidopsis Q8y6a5 listeria mc O9f1j8 arabidopsis Q96uw2 trichoderma

094ca8 arabidopsis 058755 pyrococcus

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23 HHLTEEMOKEFHYTIGPYSTPVLTIEPGDRIIVDTRDAFEGAINSEQDIPS-QLLKMPFL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-1021;
A MID-108-21366507; PubMed-11481430;
A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
A Gostard P., Berker M., Bourty M., Cadieu E., Dreano S., Gloux S.,
A Gostard P., Becker M., Bourty M., Cadieu E., Dreano S., Gloux S.,
A Godric T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Porcetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandeabol M., Weidner S., Galibert F.;
A Renard C., Thebault P., Vandeabol M., Weidner S., Galibert F.;
A Renard C., Thebault P., Vandeabol M., Weidner S.,
A Stiporhabolum mellioti strain 1021.*
BR Stiporhabolum mellioti strain 1021.*
BR Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
BR MBL; AL591789; Cac46529.1;
BR InterPos IPRO04304; FmdA_AmdA.
BR Prim, PPO3069; FmdA_AmdA.
BR Prim, PPO3069; FmdA_AmdA. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61-586-2001 (TrEMBLrel. 19, Created)
01-586-2001 (TrEMBLrel. 19, Last sequence update)
01-587-2002 (TrEMBLrel. 20, Last sequence update)
Hyp-rh-2002 (TrEMBLrel. 20, Last annotation update)
Hyp-rh-tical protein R01950.
RC1950 OR SMC04290.
RC1950 O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome.
SEQUENCE 317 AA; 33877 MW; 7705D716F6B9EE2A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 AA
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                                                                                                                                                                                                                                  Q82XT6
Q8YZM1
Q8R8R6
Q92L36
Q96VR2
Q9RYM2
Q9RYM2
Q9RYMQ
            08RCU9
094CA8
058755
                                                                            Q8Y6A5
Q9FLJ8
Q96UW2
                                                                                                                  092AL8
                                                                                                                                           Q8U4J7
Q9ENV6
Q9JUS4
Q8TD25
                                                                                                                                                                                             Q9JZP1
Q9Y772
Q97MG8
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Q8TUQ7
                                                 094AP4
09SZF0
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 NCBI_TaxID-382;
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0976p0 sulfolobus
09a553 caulobacter
09v075 pyrococcus
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Q9ury7 schizosacch
Q8y452 listeria mo
Q9sze9 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29kqn3 bacillus ha Q8r8s5 thermoanaer Q8ulv6 pyrococcus O57v26 sulfolobus
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09kqn3 bacillus ha
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                                                                                       July 3, 2003, 15:44:52 ; Search time 80 Seconds (without alignments) 844.793 Million cell updates/sec
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                                                                                                                                                      1748
1 MKWLDESIMAKRGVGAGRKP.....GNMVDPKYTVGAMLNKNLLV 328
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             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                           of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                 protein search, using sw model
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09KGN3
08R8S5
08U1V6
097V26
097EQ1
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sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
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sp_bacteriap:*
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
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Maximum DB seq length: 200000000
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Indels 42; Length 317;

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Matches
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                                                                                                                                                                                                                                                                                                            235 TPGPVTRHIDAEGYEVTTGIGS--DIMEGARAAVSGMIDILCATRGMKPEDAYMINSVCS 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 IMVNGAEKGDVLAVYIESMEPRGVDPYGICAMIPHFGGL;;GTDLTAMENDPI.PEXVRMIK 147
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NPQNGPIMVNGAEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGLTGTDLTAMLNDPTPE 14;
                                                                                                                                                                                                                                  175 AAGTTLYLPVEVEGALFSIGDTHAAGGDGEVGGTALESAMDVVLKLELVKDANLEMPRFT 234
                                                                                                                                                                                                                                                                               29 MOKEFHYTIGPYSTPVLTIEPGDRIIVDTRDAFEGAL-NSEQUIPSQLLKMPFLNPQNGP
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                                                                                                                           197 GPGSITYPLVRAPGGRLF1GDAHACQGDGEICGIAVEFASITTIKVDL1KNWQLSWPRM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 RPLEDATRIAYRDLIYWLVEDFGFEQWDAYMLLSQCGKVRLGNMVDPKYT 317
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 AA.
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SEQUENCE FROM N.A.
STRAIN=C.125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
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Pfam; PF03069; FmdA_AmdA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                         293 DIRISHIVDQPNWVV 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 32.4%
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillaceae; Bacillus.
NCBI_TaxID-86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus halodurans.
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SEQUENCE 300 AA;
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Horikoshi K.;
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LNPQNGPIMVNGAEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGLTGTDLTAM--LNDP 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 GSIIYPLVRAFGGRLFIGDAHACQGDGE1CGIAVEFASITTIKVDLIKNWQLSWPRMENA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 ENIMSIGSARPLEDATRIAYRDLIYWLVEDFGFEQWDAYMLLSQCGKVRLGNMVDPKYT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVIATIASAESLDKAVFIAVHDMAFLFKKHTDLSTEGIATLFSITGNAQISQVVDPLKT 282
                                                                                                                                                                                                                                       Bacteria, Firmicutes, Bacilius/Clostridium group, Clostridia,
Thermoanderobacteriales, Thermoanderobacteriacede, Thermoanderobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HII----FAFSKENKPAISVKSGDELEVETMDCFSNQIQSNED---KLDEMDWNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 HHLTEEMQKEFHYTIGPYSTPVLTIEPGDRIIVDTRDAFEGAINSEQDIPSQLLKMPF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                       SIRAIN-21992816; PubMed-11997336; MEDLINE-21992816; PubMed-11997336; MEDLINE-21992816; PubMed-11997336; Med S., Dong W., Yang J., Chen Y., Xue Y., Xue X., Yang E., Dong X., Ma Y., Ling L., Chen R., Wang J., Yu J., Yang H.; Chen R., Wang J., Yu J., Yang H.; Groome Ros. 12:689-70(2002): EMBL; AE0313142; AAM25099:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%; Score 355.5; DB 16; Length 299; 32.8%; Pred. No. 1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-VCI / DSM 3638 / ATCC 43587 / JCM 8422;
Welss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
"Submitted (FEE-2002) to the EMBL/GenBank/DbBJ databases.
EMRL; AE010220, AAL681223.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 AA; 31880 MW; 199068A42CD3FEA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0801V6 PRELIMINARY: PRT; 344 cm. 2801V6: 2801V6: C1-JTN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Putative formamidase (formamide amidohydrolase).
                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 124;
299 AA
                                                                Created)
PRT;
                                                                                                                                                Predicted acetamidase/formamidase.
                                                                                                                                                                                                             Thermcanaerobacter tengcongensis.
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                                                         01-JUN-2002 (TrEMBLrel. 2:,
01-JUN-2002 (TrEMB:,rel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 98; Conserv
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SECUENCE 299 AA
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235 ASITTIKVDLI----KNWQLSWPRMENAEN------IMSIGSARPLEDATR 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 PYSTPVLITEPGDRIIVDIRDAFEGAINSE---QDIPSQLLKMPFLNPQNGPIMVNGAEK 95
                                                                                                                                                                                    130 FGDLNVKVPIYPFPGVIGTGLPFRGKLSTIPPRENGGNMDIKHLIVGTKIYLEVFVNGAL
                                                                                                                                                                                                                                                                                                                                           GSARPLEDATRIAYRDLIYWLVEDFGFEQWDAYMLLSQCGKVRLGNWYD-PKYTVGAMLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIDSNLMNATKKAIRGIISILSKYMA--PVEAYILASVVVNLRVSEVVDVPNMIVTAYLP
                                                                                                                                      RHIL----PYKPHIGILSVS-PHIDSINSLIPDNHGGNMDVPDIGPGS:TYPLVRAPGGR
                                                                                                                                                                                                                                                                                         213 LFIGDABACOGDGEICGIAVEFASITTIKVDLIKNWQLSWP------RMENAENIMSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDIEPAAEVDPGDIVVIETRDALDGQITANPGVDDVASADLNV--VHPLTGPVYVRGAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 FSEDLPNVRIPGDPFLGVMGVAPSKELLKEIKEREDRLLKRGGFVLPPTPEGAVPPREPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 -- DSINSLTPDNHGGNMDVPDIGPGSITYPLVRAPGGRLFIGDAHACQGDGEICGTAVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haikawa Y.,
ai A., Kosuqi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rawarabayasi Y., Hino Y., Borikawa H., Yamazaki S., Haikawa Jin no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Ko Hescyama A., Fukui S., Nagai Y., Kishijima K., Nakazawa H., Sakamiya M., Masiada S., Punahashi T., Tanaka T., Kudoh Y., Yamazaka J., Kushida N., Oguchi T., Tanaka T., Kudoh Y., Yamazaka J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Compisete genome sequence of an aerobic hyper-thermophilic cremarchaecon, Acropyrum pernix Kl.",
EMBL. AP0003591 BAA79495.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aeropyrum pernix.
Archaea; Crenarchaeota: Thermoprotei; Desulfurococcales:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 AA; 41052 MW; 26BB63361FECE1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09YEQ1:
01-NOY-1999 (TrEMBLrel. 12, Created)
01-NOY-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
377AA iong hypothetical acetamidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 SKRH----TLPYKPHIGTLSVSP-----EI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.0%; Score 332.5; DB 1
27.8%; Pred. No. 1.4e-20;
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MEDLINE-99310339; Pubmcd-10382966;
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Pfam: PF03069; FmdA_AmdA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desuifurococcaceae; Aeropyrum
NCBI_TaxID=56636;
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Best Local Similarity
Matches 99, Conserv
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SEGGENCE 377 AA:
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29YEQ1
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SIGNIA N-ATCC 35092 / DSM 1617 / F2;

MEDLINE-21332296; PubMed=1427726;

MEDLINE-21332296; PubMed=1427726;

MANAYEZ M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curiss S.A.,

A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curiss S.A.,

A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curiss S.A.,

A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curiss S.A.,

A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curiss S.A.,

A mayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curiss S.A.,

A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G.,

A wayez M.J.,

A complete protecting W.Y.,

A complete W.Y.,

A complete protecting W.Y.,

A complete 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 VYIEGAEKGKILKVKI---LEIEVNDRGVIVTAPGAG-------VLGDLVKAPKIKVC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 KLDSEKVYWSKRHTLPYKPHIGTLSV-SPEIDSINSLTPDNHGGNMDVPDIGPGSLTYPL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 VRAPGGRLFIGDAHACQGDGBICGTAVEFASITTIKVDLIKNWQLSWPRMENAENIMSIG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEEDLEDAVREAVKOGVDII.RRANE - - - LSWDHAYMLASLIMDVQISQI,VDPRKTVRVR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 VLAVYIESMEPRGVDPYGICAMIPHFGGETGTDETAMENDPEPEKVRMIKEDSFKVYWSK 157
                                                                                                                                                                                                                                                                            31 KEFB-YTIGPYSTPVLTIRPGDR13VDTRDAFEGAJNSEQD1PSQDLKMPF--LNPQNGP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 KEKHVYSFGPDMKEVARAKPGFIIVFETLDALGGGIRSERD---TVEKIDESRVNPATGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SARPLEDATRIAYR---DLIYMLVEDFGFEOWD-AYMLLSQCGKVRLGNMVDPKYTVGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 PVLTIEPGDRIIVDTRDAFEGAI----NSEODIPSQLLKMPF--LNPQNGPIMVNGAEKSD
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                                                                                                                                                                                                     3427 1347S
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Archea: Crenarchaeota: Thermoprotei: Sulfolobaies; Sulfolobaceae:
Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                         Score 348: DB 17: Length 344;
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                                                                                                        19.9%; Score 34b; p. ...
33.7%; Pred. No. 5.6e-22; ive 49; Mismatches 122; Indels ....
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Complete proteome: Hypothetical protein.
344 AA: 37750 MW: C6GB80APF5DGF948 GR064;
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01-0CT-2001 (TrEMBLIC). 18, Last sequence update)
01-0CC-2001 (TrEMBLIC). 19, Last annotation update)
Hydrolase, acetumydase/formamidase related, pitalive.
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                                                                                                                                                           Best Local Similarity 33,74
Matches 103; Conservative
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Matches 106; Conservative
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Hydrolase;
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158 RHTL----PYKPHIGTLSVS-PEIDSINSLTPDNHGGNMDVPDIGPGSITYPLVRAPGGR 212
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Pubbed-1152470;
Rawarabayasi Y., Horikawa H., Jin-no K., Takahashi M.,
Rawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fikui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki C., Kushida N., Oquchi A.,
Aoki K.-I., Masuda S., Yanaqii M., Nishimura M., Yamaqishi A.,
Oshima T., Kikuchi H.,
                                                                                                   276 IAYRDLIYW--LVEDFGFEQWDAYMLLSQCGKVRLGNMVD-PKYTVGAMLNKNLLV 328
                                                                                                                                            SAKHALLN:INLERAGYIREQAYILASVAADLRLSQ:\UVVP\PIVTAFLPLD:F1 366
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Sulfolobus.
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Crenarchaeon, Sulfolobus tokodali strain?.";
DNA Res. 8:123-140(2010)
EMBL, Aero0098! BAB65106.1; ...
InterPro: IPR004104; FmdA_AmdA.
Ffam: PF03069; FmdA_AmdA. i.
Bypothetical protein; Complete proteome.
SEQUENCE 318 AA: 35128 MW; E0F63FED79B81255 CRC64;
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PEGUENCE FROM N.A.

RX MEDLINE-21:73698 / CR15;

RX MEDLINE-21:73698 Pubbed=11259647;

RA MISTMAN N.C., Feldblyun T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

RA BOTCOKA I., Nelson W.C., Newton A., Stephens C., Phadke N.D. Ely B.,

RA POTCOKA I., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

RA KALONAR J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA KALONAR J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA KALONAR J.F., Smit J.C., Shapiro L., Fraser C.M.;

RA SALEberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

RA SALEberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

RA "Corpore genome sequence of Caulobacter crescentus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 YLPVWVPGANFSVGDGHGRQGDGEVCVNALEMGLTGTFTFVLHKKANGAADIAPFAWPRA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 PVLTIEPGDRIIVSTRUAFEGAI-----NSEQSIPSQLLKMPFLNPQ------NGPIM 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETPTHYVLMGFHEDLDLAMKQALRQTIDFITARSNLTRVQAYQFCSLAVDFRVTQTVNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSE----KVYWSKRHILPYKPHIGTLSVSP--EIDSINSLIPDNHGGNMDVPDIGPGSIT
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Pyrococcus.
NCBI_TaxtD=29292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 3C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 AA; 32646 MW; E31FDAB7E59FD4BF CRC64;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-KAY-2000 (TTEMBLTEL. 13, Last sequence update)
01-KAY-2002 (TTEMBLTEL. 20, Last annotation update)
Hypothetical protein PAB0614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.4%; Score 322.5; DB 16; 31.7%; Pred. No. 7.8e-20; iive 41; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam: PF03069; EndA_AmdA.
Pfam: PF03069; EndA_AmdA. 1.
Complete proteome.
SEQUENCE 3AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 31.7%
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | |:|:| ||
292 KGVHALLSKGLL 303
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                                                                                                   Amidase-related protein.
                                                                                                                                                                    Caulobacter crescentus
                                                                                                                                                                                                                                                   NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus abyssi
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Similarity
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          Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 AKRGILRVDILDIKVEG-------KGAVVTAPGAGVIGKKVERPOTRICE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 idsekvywskrhtidpykphigtlsvspeidsinsliponhggnmdvpdigpgsityphvr 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 APGCRLFIGDAHACQGDGEICGTAVEFASIITIKVDLIKNWQLSWPRMENAENIMSIGSA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 RPLEDATRIAYRDLIYWLVEDFGFE-----QWD-AYMLLSQCGKVRLGNMVDPKYIV 318
                                                                                                                                                                                                                                                                                                                                                                                      35 YTIGPYSTPVLTIEPGDRIIVDIRDAFEGAINSEQDIPSQLLKMPF--LNPQNGPIMVNG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                      14 YSFGPNMKEVARAKPGEIVIFQTLDALGGQVKSEED---T:EKIDFSRVNPATGP::YVEG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAINE-9287316; Pubmed-10360571; Mills B. Dodson R.J., Dodson R.J., Malthe-9287316; Pubmed-10360571; Malthe-9287316; Pubmed-10360571; Malthe-9287316; Pubmed-10360571; Malthe-P., McDonald L., Utterback T.R., Malck J.A., Linher K.D., Garrett M.M., McDonald L., Utterback T.R., Malck J.A., Linher K.D., Garrett M.M., Beiderberg J., Sutton S.G., Facischman R.D., Elsen J.A., White C., Stayrart A.M., Cotton M.D., Venter J.C., Fraser C.M.; Salzberg S.L., Smith H.G., Venter J.C., Fraser C.M.; Salzberg S.L., Smith H.G., Venter J.C., Fraser C.M.; Springer of Thermocoga maritima.*; Mature 399:323-329(1999).

INDIA MALTER 399:323-329(1999).

INGR: MROIL99:
                                                        chromosone
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                Query Match 17.4% Score 304.5; DB 17; Length 299; Best Local Similarity 30.7%, Fred. No. 2.8e-18; Matches 94; Conservative 45; Mismatches 120; Indels 47;
                                                        into archaeal
                                                                      Structure and evolution.";
Submitted (JUL-1999) to the EMEL/GenBank/DDBJ databases.
EMBL; AL246285; CAR4948(0.1;
Interpro; IPROJ4304; FmdA_AmdA.
Fiam; PPO3069; FmdA_AmdA.
Hypothetical protein: Complete proteome.
SEQUENCE 298 AA: 32456 MW; 47CF8AD3C33G2E22 CRC64;
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Last annotation update)
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                          Heilig R.; "Pyrococcus abyssi genome sequence: insights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 AA
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Pfam; PF03069; FmdA_AmdA: 1.
Complete proteome.
SEQUENCE 285 AA; 31196 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acetamidase, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 RVRIPK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ihermotoga maritima
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61 VRPGDTLKVRIKRIELPR----RGMIVTGKGFG------VLGDEV-EGFHIKELBIE 136
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                                                                                                                                                                                                                                                 93 AEKGDVLAVYIESM-LPRGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSE 151
                                                                                                                                                                                                                                                                                                                                                                                                 152 KVYWSKRH---TLPYKPHIGTLSVSPEJDSINS:JPDNHGGNMDVPDJGPGSITYPLVRA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 PGGKLFIGDAHACQGDGEIGGTAVEFASITTIKVDLIKNWQUSWPRMENAFNIMSIGSAR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 MPFI.N-----PQ-----NGPIMVNGAEKGDVLAVYIESMI.PRGVDPYGICAMIP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 HFGGLTGTDLTAMLNDPLPEKVRMIKL----DSEKVYWSKRHTLPYKPHIGTLSVSPEID 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 GWG-----ALPNOFTQPALRFIPLNLANNTAEFPPNSGIKIPLTPFFGILGVATPEN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 K--WAVIJEDGVRIPIHPMVGVIGVAPQEGEYPTGTAHRHGGNMDIKEITENVTVHLPVFQ 164
                                                                                                                                                       21 VTHELTEEMQKEFHYTIGPYS---TPVLJIEPGDRIIVDIRDAFEGAINSEQDIPSQLLK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 YTLGPYSTPVLTIEPGDRIIVDTRDAFEGAINSEQDIPSQLLKMPF--LNPQNGPIMVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SINSLTPDNHGGNMDVPDIGPGSITYPLVRAPGGRLFIGDAHACQGDGEICGTAVEFASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 DIEEALKEVTRETVWFIORRKTIPFIDAYMLASLSVDVGISQLVNPAKTAKARIPK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 PEEDATRIAYRDLIYWLVEDFGFEQWDAYMLLSOCGKVRLGNMVDPKYTVGAMLNK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJUS-21595285; PubMed-1.759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Itjuchi M., Ishikawa A., Kawashima K., Kimura T., Kishda Y., Kohara W., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Pabata S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Yasuda S., Sugimoto M., Takazawa M., Yamada M., Yasuda S., Sugimoto M., Takazawa M., Yamada M., Yasuda S., Sugimoto M., Takazawa M., Yamada M., Yasuda S., Surain PCC 7120.",
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29.7%; Pred. No. 5.8e-18;
tive 53; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anabaena sp. (strain PCC 7120).
Bacteria: Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCB_TaxiD=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESFBAUE4AF4165D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (T-EMBLrel, 20, Created)
01-MAR-2002 (TrEMBLrel, 20, Last sequence update)
01-JUN-2002 (TrEMBLrel, 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328
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InterPro: 1PR04304; FmdA_AmdA.
Frant : PF0706918 FmdA_AmdA.
Pypetherical protein; Complete proteome.
SEGUENCE 328 AA; 35627 MW; DESTBA0E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein All0706.
ALL0706.
                                     85; Conservative
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West Local Similarity
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01-JUN-2001 (
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                                 43 PVLTIEPGDRIIVDTRDAFEGAINSEQDIPSQLEKMPFENPQNGPTMVNGAEKGDVLAVY 102
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238 TTIKVDLIKNWQLSWPRMENAENIMSIGSARPLEDATRIAYRDLIYWLVEDFGFEGWDAY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diaser P., Franceul L., Buchrieser C., Rushiok C., Amend A., Baquero F., Berche P., Blocker H., Brandt P., Chakraborty T., Chatchard E., Couve E., de Dartwar A., Deboux P., Domann E., Dominguez Bernal G., Duchaud E., Purrant L., Dominguez Bernal G., Duchaud E., Purrant L., Bussurget D., Burtian K.-D., Fsini H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson E., Jones L.-M., Kaerst U., Kreft J., Kunst F., Kursker G., Maduero E., Maitournam A., Mara Viceite J., Ng E., Nodjari H., Nordsiek G., Novella S., de Pablos B., Perez-filaz J.-C., Purcell k., Requez-Boland J.-A., Voss H., Wehland J., Cossart P., Comparative genomics of Listeria species."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.0%; Score 261.5; DB 16; Length 299; 29.0%; Pred. No. 1.5e-14; ive 44; Mismatches 112; Indeis 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Firmicutes, Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 294:849-852(2001).
EMBL. ALS96173. CA65978 ...
LISTLIAS. LIN02752.
InterPro: IPR004304; Fwda_Amda.
Priam; PF03069; Fmda_Amda: 1.
Protein: 299 As. 33:83 MW: B79878A0B90A70D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLE) 19, Last sequence update) 01-5UN-2002 (TrEMBLE) 19, Last senctation update) 10-5UN-2002 (TrEMBLE) 21, Last annotation update) Hypothetical protein lin2752.
Listeria innocua.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 TEKATKKALONMLNVLMESDKITLEDAIFLLS 267
                                                                                                                                                                                                                                                                                                               299 AA
                                                                                                            298 MLLSQCGKVRLGNMVD-PKYTVGAMLNKNE 326
                                                                                                                                                   01-DEC-2001 (TrEMBLrel, 19, Created)
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STRAIN~CLIP 11262 / SEROVAR 6A;
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NCBI_TaxID~1642;
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Matches
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RESULT 13 09C453

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GPIMVNGAEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGLTGTULTAMLNDPLPEKVRM 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----NHGGNMDVPDIGPGSITYPLVRAP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGRLFIGDAHACQGDGE1 - - CGTAVEFASITTIKVDLIKNWQLSWPRMENAENIMSIGSA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 OKEFHYTIGPYSTPVLTLEPGDRIIVDTRDAFEGAI---NSEQDIPS-QLLKMPFLNPQN 85
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Bost Local Similarity 25.5%; Pred. No. 1.9c-12;
Matches 95; Conservative 45; Mismatches 123; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Traser J.A., Davis M.A., Hynes M.J.;
"The Formamidase Gene of Aspergillus nidulans: Regulation by I Metabolite Repression and Transcriptional Interference by an Goverlapping Upstream Gene.";
Generics 157:119-131(2001).

"MBL, AF274009; AAG60585.1; -.
InterPro: IPR004304; FmdA_AmdA.

Pfam; PF03069; FmdA_AmdA.

Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Fungi; Ascomycota: Pezizomycotina: Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
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SPAC869.04.
SPAC869.04.
Bukaryota: Fungi, Ascomycota: Schizosaccharomycetes; Schizosaccharomycetes; Schizosaccharomycetacea; Schizosaccharomycetacea; Schizosaccharomycetacea; Schizosaccharomycetacea; Schizosaccharomycetaceae;
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Last annotation update)
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Last annotation update)
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MEDLINE=21066161; Pubmed-11139496;
                                                                                              01-JJN-2001 (TrEMBLrel, 17, 01-JJN-2001 (TrEMBLrel, 17, 01-JUN-2002 (TrEMBLrel, 21, Formanidase (EC 3.5.1.49).
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361 CAPVQCHIAGLVD 373
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PRELIMINARY;
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102 YIESMLPRGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRH-- 159
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KA MEDLIKE-21537279; PubMed=116/9669;

R Glaser P. Frangeul L., Buchrieser C., Rusnick C., Amend A.,

Glaser P. Frangeul L., Buchrieser C., Rusnick C., Amend A.,

Baquero F., Berthe P., Bloeker B., Brandt P., Chakaborry T.,

R Charbit A., Chetcuani F., Ccuve E., de Dauvar A., Deboux P.,

R Charbit A., Chetcuani F., Ccuve E., de Dauvar A., Dessurget C.,

A Domann E., Dominquez-Bernal G., Duchaud E., Durant L.,

A Gautier L., Goobel W., Gomez-Lopez N., Hain T., Hauf C., Jackson D.,

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A Madheno E., Maltournam A., Maha Vicente J., My E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simose N., Tierrez A.,

A Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

"Comperative genomics of Listeria species.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 GKOHYLCTTTAYROTCLRVIHYFRRFGYNDYOLYLLLS-CAPIOGHVAGIVD 372
SEQUENCE FROM N.A.
STRAIN-972H-:
Nunt. C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
Nunt. C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
Submitted (NOV-1999) to the FMBL/GenBack/DoBG databases.
EMBL: AL132779; CABGSG14 11;
Interpro; IPPG04304; FmdA_AmdA.
SEQUENCE 410 AA: 44792 MW; D4427AG222925D36 CRC64;
                                                                                                                                                                                                                              97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Listeria monocytogenes.
Bacteria, Firmicutes, Bacillus/Clostridium group: Bacillales;
Listeriaceae: Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                        Length 410;
                                                                                                                                                                                      15.4%; Score 233.5; DB 3; Length 25.1%; Pred. No. 6.3e-12; ive 48; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51-WAR-2002 (TFEMBLREL. 20. Created)
50-WAR-2002 (TFEMBLREL. 20. Last sequence update)
61-53N-2002 (TFEMBLREL. 21. Last annotation update)
Hypothetical protein Imo2603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete proteome.
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EMBL, AL51983: CAD00681.1: -
Listilist; LM002663: -
InterPro; IPR004304; Fmda_Amda.
                                                                                                                                                                               Query Match
Best Local Similarity 25.1%
Matches 92, Conservative
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114 VENNOIIYSEDIHIPIRKTIGLL----KTEELNPSKVPIKNGGLLDSSKITEGATIFLPV 169
                                                                                                                                                                                                                                                                                                                                                                           207 RAPGGRIFIGDAHACQGDGEICGIAVEFASITIIKVDLIKNWQLSWPRMENAENIMSIGS 266
                                                                                                                                                                                                                                                                                                                                                                                                                     170 EKYGASLHVGNVRATTGFGKITATSAEAPAEVTLKLQILKNRTAPTFTIIHYHNLICLAS 229
                                                                                                                                                                                                            98 TMYNGAEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIK 147
                                                                                                                                                                                                                                                                                               148 LDSEKVYWSKRHTLPYKPHIGTLSVSPEIDSIN~SLTPUNHGGNMDVPDIGPGSITYPLV 206
                                                                                                                        67
                                                                                                                                                                    63
                                                                                                                          28 ENOKEFHYTIGPYSTPVLTIEPGDRIJVDTRDAFEGAINSEQDIPSQLLKMPFLNPONGP
                                                                                                                                                                    13 EMEKS-----TEPAIRVKDGSVVK:KTKDHFNGQIHAKQLHYGELDWKQF-SPTTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 ARPLEDATRIAYRDLIYWLVEDFGFEQWDAYMLLSQCGKVRLGNMVDPKYIVGAML 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 DITIEKATOKTMHNMITI, LTESPKMTTEDALFLISLOADFOVCKLCKPNITTSIKL 285
                                                                                  Gaps
                                                                                24;
                                     Length 296;
                                                                                  [ndels
063D97A94F440816 CRC64;
                               Query Match
Hest Local Similarity 25.0%; Pred. No. 4.4c ____
Matches 74; Conservative 52; Mismatches 136;
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296 AA; 32959 KW;
  SECOENCE
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